



SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: BIOGEN, INC.
- (ii) TITLE OF INVENTION: Ret Ligand (RetL) for Stimulating Neural and Renal Growth
- (iii) NUMBER OF SEQUENCES: 21
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Biogen, Inc.
 - (B) STREET: 14 Cambridge Center
 - (C) CITY: Cambridge
 - (D) STATE: MA
 - (E) COUNTRY: USA
 - (F) ZIP: 02142
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER:
 - (B) FILING DATE: 07-MAY-1997
 - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 08/999,999
 - (B) FILING DATE: 01-JAN-1996
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Levine, Leslie M.
 - (B) REGISTRATION NUMBER: 35,245
 - (C) REFERENCE/DOCKET NUMBER: A008 PCT CIP
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: 617-679-2400
 - (B) TELEFAX: 617-679-2838

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 3616 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 257..1660

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

60 GCGGCCGCAG GTTGGGTCGG AACTGAACCC CTGAAAGCGG GTCCGCCTCC CGCCCTCGCG
120 CCCGCCCGGA TCTGAGTCGC TGGCGGCGGT GGGCGGCAGA GCGACGGGGA GTCTGCTCTC
180 ACCCTGGATG GAGCTGAACT TTGAGTGGCC AGAGGAGCGC AGTCGCCCCG GGATCGCTGC
240 ACGCTGAGCT CTCTCCCCGA GACCGGGCGG CGGCTTTGGA TTTTGGGGGG GCGGGGACCA
289 GCTGCGCGGC GGCACC ATG TTC CTA GCC ACT CTG TAC TTC GCG CTG CCA
Met Phe Leu Ala Thr Leu Tyr Phe Ala Leu Pro
1 5 10
337 CTC CTG GAT TTG CTG ATG TCC GCC GAG GTG AGT GGT GGA GAC CGT CTG
Leu Leu Asp Leu Leu Met Ser Ala Glu Val Ser Gly Gly Asp Arg Leu
15 20 25
385 GAC TGT GTG AAA GCC AGC GAT CAG TGC CTG AAG GAA CAG AGC TGC AGC
Asp Cys Val Lys Ala Ser Asp Gln Cys Leu Lys Glu Gln Ser Cys Ser
30 35 40
433 ACC AAG TAC CGC ACA CTA AGG CAG TGC GTG GCG GGC AAG GAA ACC AAC
Thr Lys Tyr Arg Thr Leu Arg Gln Cys Val Ala Gly Lys Glu Thr Asn
45 50 55
481 TTC AGC CTG ACA TCC GGC CTT GAG GCC AAG GAT GAG TGC CGT AGC GCC
Phe Ser Leu Thr Ser Gly Leu Glu Ala Lys Asp Glu Cys Arg Ser Ala
60 65 70 75
529 ATG GAG GCC TTG AAG CAG AAG TCT CTG TAC AAC TGC CGC TGC AAG CGG
Met Glu Ala Leu Lys Gln Lys Ser Leu Tyr Asn Cys Arg Cys Lys Arg
80 85 90
577 GGC ATG AAG AAA GAG AAG AAT TGT CTG CGT ATC TAC TGG AGC ATG TAC
Gly Met Lys Lys Glu Lys Asn Cys Leu Arg Ile Tyr Trp Ser Met Tyr
95 100 105
625 CAG AGC CTG CAG GGA AAT GAC CTC CTG GAA GAT TCC CCG TAT GAG CCG
Gln Ser Leu Gln Gly Asn Asp Leu Leu Glu Asp Ser Pro Tyr Glu Pro
110 115 120
673 GTT AAC AGC AGG TTG TCA GAT ATA TTC CGG GCA GTC CCG TTC ATA TCA
Val Asn Ser Arg Leu Ser Asp Ile Phe Arg Ala Val Pro Phe Ile Ser
125 130 135
721 GAT GTT TTC CAG CAA GTG GAA CAC ATT TCC AAA GGG AAC AAC TGC CTG
Asp Val Phe Gln Gln Val Glu His Ile Ser Lys Gly Asn Asn Cys Leu
140 145 150 155

769 GAC GCA GCC AAG GCC TGC AAC CTG GAC GAC ACC TGT AAG AAG TAC AGG
 Asp Ala Ala Lys Ala Cys Asn Leu Asp Asp Thr Cys Lys Lys Tyr Arg
 160 165 170

817 TCG GCC TAC ATC ACC CCC TGC ACC ACC AGC ATG TCC AAC GAG GTC TGC
 Ser Ala Tyr Ile Thr Pro Cys Thr Thr Ser Met Ser Asn Glu Val Cys
 175 180 185

865 AAC CGC CGT AAG TGC CAC AAG GCC CTC AGG CAG TTC TTC GAC AAG GTT
 Asn Arg Arg Lys Cys His Lys Ala Leu Arg Gln Phe Phe Asp Lys Val
 190 195 200

913 CCG GCC AAG CAC AGC TAC GGG ATG CTC TTC TGC TCC TGC CGG GAC ATC
 Pro Ala Lys His Ser Tyr Gly Met Leu Phe Cys Ser Cys Arg Asp Ile
 205 210 215

961 GCC TGC ACC GAG CGG CGG CGA CAG ACT ATC GTC CCC GTG TGC TCC TAT
 Ala Cys Thr Glu Arg Arg Arg Gln Thr Ile Val Pro Val Cys Ser Tyr
 220 225 230 235

1009 GAA GAA CGA GAG AGG CCC AAC TGC CTG AGT CTG CAA GAC TCC TGC AAG
 Glu Glu Arg Glu Arg Pro Asn Cys Leu Ser Leu Gln Asp Ser Cys Lys
 240 245 250

1057 ACC AAT TAC ATC TGC AGA TCT CGC CTT GCA GAT TTT TTT ACC AAC TGC
 Thr Asn Tyr Ile Cys Arg Ser Arg Leu Ala Asp Phe Phe Thr Asn Cys
 255 260 265

1105 CAG CCA GAG TCA AGG TCT GTC AGC AAC TGT CTT AAG GAG AAC TAC GCA
 Gln Pro Glu Ser Arg Ser Val Ser Asn Cys Leu Lys Glu Asn Tyr Ala
 270 275 280

1153 GAC TGC CTC CTG GCC TAC TCG GGA CTG ATT GGC ACA GTC ATG ACT CCC
 Asp Cys Leu Leu Ala Tyr Ser Gly Leu Ile Gly Thr Val Met Thr Pro
 285 290 295

1201 AAC TAC GTA GAC TCC AGC AGC CTC AGC GTG GCA CCA TGG TGT GAC TGC
 Asn Tyr Val Asp Ser Ser Ser Leu Ser Val Ala Pro Trp Cys Asp Cys
 300 305 310 315

1249 AGC AAC AGC GGC AAT GAC CTG GAA GAC TGC TTG AAA TTT CTG AAT TTT
 Ser Asn Ser Gly Asn Asp Leu Glu Asp Cys Leu Lys Phe Leu Asn Phe
 320 325 330

1297 TTT AAG GAC AAT ACT TGT CTC AAA AAT GCA ATT CAA GCC TTT GGC AAT
 Phe Lys Asp Asn Thr Cys Leu Lys Asn Ala Ile Gln Ala Phe Gly Asn
 335 340 345

1345 GGC TCA GAT GTG ACC ATG TGG CAG CCA GCC CCT CCA GTC CAG ACC ACC
 Gly Ser Asp Val Thr Met Trp Gln Pro Ala Pro Pro Val Gln Thr Thr
 350 355 360

1393 ACT GCC ACC ACT ACC ACT GCC TTC CGG GTC AAG AAC AAG CCT CTG GGG
 Thr Ala Thr Thr Thr Thr Ala Phe Arg Val Lys Asn Lys Pro Leu Gly
 365 370 375
 1441 CCA GCA GGG TCT GAG AAT GAG ATC CCC ACA CAC GTT TTA CCA CCC TGT
 Pro Ala Gly Ser Glu Asn Glu Ile Pro Thr His Val Leu Pro Pro Cys
 380 385 390 395
 1489 GCG AAT TTG CAG GCT CAG AAG CTG AAA TCC AAT GTG TCG GGT AGC ACA
 Ala Asn Leu Gln Ala Gln Lys Leu Lys Ser Asn Val Ser Gly Ser Thr
 400 405 410
 1537 CAC CTC TGT CTT TCT GAT AGT GAT TTC GGA AAG GAT GGT CTC GCT GGT
 His Leu Cys Leu Ser Asp Ser Asp Phe Gly Lys Asp Gly Leu Ala Gly
 415 420 425
 1585 GCC TCC AGC CAC ATA ACC ACA AAA TCA ATG GCT GCT CCT CCC AGC TGC
 Ala Ser Ser His Ile Thr Thr Lys Ser Met Ala Ala Pro Pro Ser Cys
 430 435 440
 1633 AGT CTG AGC TCA CTG CCG GTG CTG ATG CTC ACC GCC CTT GCT GCC CTG
 Ser Leu Ser Ser Leu Pro Val Leu Met Leu Thr Ala Leu Ala Ala Leu
 445 450 455
 1680 TTA TCT GTA TCG TTG GCA GAA ACG TCG TAGCTGCATC CGGGAAAACA
 Leu Ser Val Ser Leu Ala Glu Thr Ser
 460 465
 1740 GTATGAAAAG ACAAAGAGA ACCAAGTATT CTGTCCCTGT CCTCTTGAT ATCTGAAAAT
 1800 CCAGTTTAA AAGCTCCGTT GAGAAGCAGT TTCACCCAAC TGGAACCTT TCCTTGTTTT
 1860 TAAGAAAGCT TGTGGCCCTC AGGGGCTTCT GTTGAAGAAC TGCTACAGGG CTAATTCCAA
 1920 ACCCATAAGG CTCTGGGGCG TGGTGCGGCT TAAGGGGACC ATTTGCACCA TGTAAGCAA
 1980 GCTGGGCTTA TCATGTGTTT GATGGTGAGG ATGGTAGTGG TGATGATGAT GGTAATTTTA
 2040 ACAGCTTGAA CCCTGTCTC TCTACTGGTT AGGAACAGGA GATACTATTG ATAAAGATTC
 2100 TTCCATGTCT TACTCAGCAG CATTGCCTTC TGAAGACAGG CCCGCAGCCT AGTGTGAATG
 2160 ACAAGTGGAG GTTGGCCTCA AGAGTGGACT TGGCAGACTC TACCTTGATG TAATGTTTAC
 2220 CTTTCCGTGT ATGGTCTCCA CAGAGTGTTT ATGTATTTAC AGACTGTTCT GTGATCCCCC
 2280 AACAACAACA ACCACAAATT CCTTGGTCAC CTCCAAATGT AACCGGTCCT TTAGCCCAGT

2340 AGAGGAGGGT GGGTGTGGCC CTGGCACAGC TCCCGGATTG TTGATGGGCA CTCTCCTGAG
 2400 CTTTGCTTGA GTGAGAAGCT GAATGTAGCT GAAAATCAAC TCTTCTTACA CTTCTTACTG
 2460 CTTTCGTTTAC TTACGAGGTC ACATATAGAA CAAACATCAC CAACTATTAG CTTACCGTTA
 2520 GCTTCCCAAC TATTAGCTTT CTATGTTTTG AAAGCAGTGT TGCTGACCCC ATGTTTTAAT
 2580 GATGGTTTAA TACATGCAGC CCTTTCCTCT CATCGGTAAC ACTAGCTCCA ACATCAACTT
 2640 CATGCATGTG GCTCTCAAAA GCAGGCCCCA AGAAGCCCAG TTCTTTAGGA GAAAGCTGCG
 2700 TCCTGTTTCT GTGGACAGGC AGGAGGAAAC AGAGCAGCCT GCCCGTGGTG TCTTTATCTG
 2760 TTTTGAAATC AAGGCTGCCT GTGTGTAAGG AATGGTTCAA TTCTTATAAA GGGTGCCACT
 2820 GTTGATGCCA CAACTGGCAG TTGGTCTAGC TCCAGGACAC CGGTTTCCAT GTTGCTGGC
 2880 AGAGACAGCT TTGATTGGGA CTGGCTGGCC ACAAGGGATG GGATGAAGAT GTGCTGCCCT
 2940 CTCTTTCAAA GTTGAGCCCT GCCAGGGCAC ATAGAAGCAT CTTTGCTCCT GACCACAACG
 3000 TAGAACAGCT TGGATTCAAG GTCATCAAGC GTCTCCTGTA CATTGCTCTG TGACCTTCAT
 3060 AACAGACTGT CCCGCACAAA AGGAACGGCA GTTTATGGAT CTAGAGTGGG AGCACAGGGT
 3120 CTGGAAAGGT GAACCGATTG GCAAAATACA CAGAACAGGA GGGAGAGTCT CAAGCCGAGA
 3180 CATCTTGCTT ACTAGCCACA CACCATCTCC TGGAGCCCTC TCCTGACCT GGGCAGACCC
 3240 TTAGGTGTAT ATCTAAAGAC CTCTTCAATG TTCAGGTTC AATCTGTAA ATGGTTGCGT
 3300 CCTGGCACCC ATTCTGAAA ACTGAACAAA GGAGAGGATA TCTTTCCTCC ATTGAGCCCT
 3360 GAAAGTATGA CTGGCTTCTC ACCCTCCAC AGAGCAGGGA GCCCTGGTGC ACACAGTCTC
 3420 CTGATATCCT CCCTGCTCTT TGAGGTTTGC CTTGGGAGAA AATGATTAC CTCGGGAGGG
 3480 GACGCTTTGG TGTCTGAAGT ACGTTTATAT CGAAATGTTA ATGAATACCC ATGTAAAATA
 3540 CTCAATAGCC ACCTTCTTC CCTTCACAAT GTTTTCGAGG GGAATGCATC CAACATCCAA
 3600 GTGTACCTGG TCAGTGGGAA GTTCCATGAA GACTCATACA TTGAATAAAC ATATTGATG

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 468 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met 1	Phe	Leu	Ala	Thr 5	Leu	Tyr	Phe	Ala	Leu 10	Pro	Leu	Leu	Asp	Leu 15	Leu
Met	Ser	Ala	Glu 20	Val	Ser	Gly	Gly	Asp 25	Arg	Leu	Asp	Cys	Val 30	Lys	Ala
Ser	Asp	Gln 35	Cys	Leu	Lys	Glu	Gln 40	Ser	Cys	Ser	Thr	Lys 45	Tyr	Arg	Thr
Leu	Arg 50	Gln	Cys	Val	Ala	Gly 55	Lys	Glu	Thr	Asn	Phe 60	Ser	Leu	Thr	Ser
Gly 65	Leu	Glu	Ala	Lys	Asp 70	Glu	Cys	Arg	Ser	Ala 75	Met	Glu	Ala	Leu	Lys 80
Gln	Lys	Ser	Leu	Tyr 85	Asn	Cys	Arg	Cys	Lys 90	Arg	Gly	Met	Lys	Lys 95	Glu
Lys	Asn	Cys	Leu 100	Arg	Ile	Tyr	Trp	Ser 105	Met	Tyr	Gln	Ser	Leu 110	Gln	Gly
Asn	Asp	Leu 115	Leu	Glu	Asp	Ser	Pro 120	Tyr	Glu	Pro	Val	Asn 125	Ser	Arg	Leu
Ser	Asp 130	Ile	Phe	Arg	Ala	Val 135	Pro	Phe	Ile	Ser	Asp 140	Val	Phe	Gln	Gln
Val 145	Glu	His	Ile	Ser	Lys 150	Gly	Asn	Asn	Cys	Leu 155	Asp	Ala	Ala	Lys	Ala 160
Cys	Asn	Leu	Asp	Asp 165	Thr	Cys	Lys	Lys	Tyr 170	Arg	Ser	Ala	Tyr	Ile 175	Thr
Pro	Cys	Thr 180	Thr	Ser	Met	Ser	Asn	Glu 185	Val	Cys	Asn	Arg	Arg 190	Lys	Cys
His	Lys	Ala 195	Leu	Arg	Gln	Phe	Phe 200	Asp	Lys	Val	Pro	Ala 205	Lys	His	Ser
Tyr	Gly 210	Met	Leu	Phe	Cys	Ser 215	Cys	Arg	Asp	Ile	Ala 220	Cys	Thr	Glu	Arg
Arg 225	Arg	Gln	Thr	Ile	Val 230	Pro	Val	Cys	Ser	Tyr 235	Glu	Glu	Arg	Glu	Arg 240
Pro	Asn	Cys	Leu	Ser 245	Leu	Gln	Asp	Ser	Cys 250	Lys	Thr	Asn	Tyr	Ile 255	Cys
Arg	Ser	Arg	Leu	Ala	Asp	Phe	Phe	Thr	Asn	Cys	Gln	Pro	Glu	Ser	Arg

260					265					270					
Ser	Val	Ser	Asn	Cys	Leu	Lys	Glu	Asn	Tyr	Ala	Asp	Cys	Leu	Leu	Ala
		275					280					285			
Tyr	Ser	Gly	Leu	Ile	Gly	Thr	Val	Met	Thr	Pro	Asn	Tyr	Val	Asp	Ser
	290					295					300				
Ser	Ser	Leu	Ser	Val	Ala	Pro	Trp	Cys	Asp	Cys	Ser	Asn	Ser	Gly	Asn
305					310					315					320
Asp	Leu	Glu	Asp	Cys	Leu	Lys	Phe	Leu	Asn	Phe	Phe	Lys	Asp	Asn	Thr
				325					330					335	
Cys	Leu	Lys	Asn	Ala	Ile	Gln	Ala	Phe	Gly	Asn	Gly	Ser	Asp	Val	Thr
			340					345					350		
Met	Trp	Gln	Pro	Ala	Pro	Pro	Val	Gln	Thr	Thr	Thr	Ala	Thr	Thr	Thr
		355					360					365			
Thr	Ala	Phe	Arg	Val	Lys	Asn	Lys	Pro	Leu	Gly	Pro	Ala	Gly	Ser	Glu
	370					375					380				
Asn	Glu	Ile	Pro	Thr	His	Val	Leu	Pro	Pro	Cys	Ala	Asn	Leu	Gln	Ala
385					390					395					400
Gln	Lys	Leu	Lys	Ser	Asn	Val	Ser	Gly	Ser	Thr	His	Leu	Cys	Leu	Ser
				405					410					415	
Asp	Ser	Asp	Phe	Gly	Lys	Asp	Gly	Leu	Ala	Gly	Ala	Ser	Ser	His	Ile
			420					425					430		
Thr	Thr	Lys	Ser	Met	Ala	Ala	Pro	Pro	Ser	Cys	Ser	Leu	Ser	Ser	Leu
		435					440					445			
Pro	Val	Leu	Met	Leu	Thr	Ala	Leu	Ala	Ala	Leu	Leu	Ser	Val	Ser	Leu
	450					455					460				
Ala	Glu	Thr	Ser												
465															

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 39 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

AAGGAAAAAA GCGGCCGCCA TGGCGAAGGC GACGTCCGG

39

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 33 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

33 AGTTTGTGTCG ACCGTGCGGC ACAGCTCGTC GCA

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 33 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

33 AGTTTGTGTCG ACCGTGCGGC ACAGCGCATC ACA

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1926 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 10..1920

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

48 GCGGCCGCC ATG GCG AAG GCG ACG TCC GGC GCC GCA GGG CTG GGG CTG

Met Ala Lys Ala Thr Ser Gly Ala Ala Gly Leu Gly Leu
470 475 480

96 AAG CTG TTT TTG CTG CTG CCG CTA CTG GGA GAA GCC CCG CTG GGT CTC

Lys Leu Phe Leu Leu Leu Pro Leu Leu Gly Glu Ala Pro Leu Gly Leu
485 490 495

144 TAC TTC TCA AGG GAT GCT TAC TGG GAG AGG CTG TAT GTG GAC CAG CCA

Tyr Phe Ser Arg Asp Ala Tyr Trp Glu Arg Leu Tyr Val Asp Gln Pro
500 505 510

192 GCT GGC ACA CCT CTG CTC TAT GTC CAT GCC CTA CGG GAT GCC CCT GGA

Ala Gly Thr Pro Leu Leu Tyr Val His Ala Leu Arg Asp Ala Pro Gly
 515 520 525
 240 GAA GTG CCC AGC TTC CGC CTG GGC CAG TAT CTC TAT GGC GTC TAC CGC
 Glu Val Pro Ser Phe Arg Leu Gly Gln Tyr Leu Tyr Gly Val Tyr Arg
 530 535 540 545
 288 ACG CGT CTG CAT GAG AAT GAC TGG ATC CAC ATC GAT GCG GGC ACT GGC
 Thr Arg Leu His Glu Asn Asp Trp Ile His Ile Asp Ala Gly Thr Gly
 550 555 560
 336 CTC CTC TAC CTC AAT CAG AGC CTG GAC CAT AGT TCC TGG GAG CAG CTC
 Leu Leu Tyr Leu Asn Gln Ser Leu Asp His Ser Ser Trp Glu Gln Leu
 565 570 575
 384 AGC ATC CGA AAT GGC GGC TTC CCC TTG CTC ACC GTC TTC CTC CAG GTC
 Ser Ile Arg Asn Gly Gly Phe Pro Leu Leu Thr Val Phe Leu Gln Val
 580 585 590
 432 TTC CTG GGG TCC ACA GCC CAG AGA GAG GGA GAG TGT CAT TGG CCA GGC
 Phe Leu Gly Ser Thr Ala Gln Arg Glu Gly Glu Cys His Trp Pro Gly
 595 600 605
 480 TGT GCC CGT GTG TAC TTC TCC TTC ATC AAC GAC ACC TTC CCA AAT TGT
 Cys Ala Arg Val Tyr Phe Ser Phe Ile Asn Asp Thr Phe Pro Asn Cys
 610 615 620 625
 528 AGC TCC TTC AAA GCC CGG GAT CTC TGC ACC CCA GAG ACG GGT GTG TCC
 Ser Ser Phe Lys Ala Arg Asp Leu Cys Thr Pro Glu Thr Gly Val Ser
 630 635 640
 576 TTC CGC ATC AGG GAG AAC AGG CCC CCT GGC ACC TTC TAC CAG TTC CGC
 Phe Arg Ile Arg Glu Asn Arg Pro Pro Gly Thr Phe Tyr Gln Phe Arg
 645 650 655
 624 ATG CTA CCT GTG CAG TTC CTT TGT CCT AAC ATC AGT GTG AAG TAC AAA
 Met Leu Pro Val Gln Phe Leu Cys Pro Asn Ile Ser Val Lys Tyr Lys
 660 665 670
 672 CTC TTA GAA GGG GAC GGT CTG CCC TTC CGT TGT GAC CCC GAC TGT CTG
 Leu Leu Glu Gly Asp Gly Leu Pro Phe Arg Cys Asp Pro Asp Cys Leu
 675 680 685
 720 GAG GTG AGC ACG CGG TGG GCA CTG GAT CGG GAG CTT CAG GAG AAG TAT
 Glu Val Ser Thr Arg Trp Ala Leu Asp Arg Glu Leu Gln Glu Lys Tyr
 690 695 700 705
 768 GTG CTG GAG GCT GAG TGC GCA GTG GCA GGC CCT GGA GCC AAC AAG GAG
 Val Leu Glu Ala Glu Cys Ala Val Ala Gly Pro Gly Ala Asn Lys Glu
 710 715 720
 816 AAG GTG GCC GTG TCC TTC CCG GTG ACG GTG TAT GAT GAA GAC GAC TCC

Lys Val Ala Val Ser Phe Pro Val Thr Val Tyr Asp Glu Asp Asp Ser
 725 730 735
 864 CCG CCC ACC TTC TCC GGA GGT GTG GGC ACC GCC AGT GCT GTG GTG GAG
 Pro Pro Thr Phe Ser Gly Gly Val Gly Thr Ala Ser Ala Val Val Glu
 740 745 750
 912 TTT AAG CGG AAG GAG GGC ACT GTG GTA GCC ACT CTG CAG GTG TTT GAT
 Phe Lys Arg Lys Glu Gly Thr Val Val Ala Thr Leu Gln Val Phe Asp
 755 760 765
 960 GCA GAT GTG GTG CCA GCA TCT GGG GAG CTG GTG AGG CGG TAC ACA AGC
 Ala Asp Val Val Pro Ala Ser Gly Glu Leu Val Arg Arg Tyr Thr Ser
 770 775 780 785
 1008 ACA CTA CTC TCA GGG GAT TCC TGG GCC CAG CAG ACC TTC CGG GTG GAG
 Thr Leu Leu Ser Gly Asp Ser Trp Ala Gln Gln Thr Phe Arg Val Glu
 790 795 800
 1056 CAC ACA CCC AAC GAG ACC TTG GTC CAG TCC AAC AAC AAC TCC GTG CGG
 His Thr Pro Asn Glu Thr Leu Val Gln Ser Asn Asn Asn Ser Val Arg
 805 810 815
 1104 GCA ACC ATG CAC AAT TAC AAG CTG GTT CTC AAC AGG AGC CTG TCC ATC
 Ala Thr Met His Asn Tyr Lys Leu Val Leu Asn Arg Ser Leu Ser Ile
 820 825 830
 1152 TCA GAG AGC CGA GTC CTG CAG CTA GTA GTC CTG GTC AAT GAC TCA GAC
 Ser Glu Ser Arg Val Leu Gln Leu Val Val Leu Val Asn Asp Ser Asp
 835 840 845
 1200 TTC CAG GGG CCT GGG TCA GGT GGT CTC TTC CTC CAT TTC AAC GTG TCT
 Phe Gln Gly Pro Gly Ser Gly Val Leu Phe Leu His Phe Asn Val Ser
 850 855 860 865
 1248 GTG CTG CCT GTC ACC CTG AAC CTA CCC ATG GCC TAC TCC TTC CCA GTG
 Val Leu Pro Val Thr Leu Asn Leu Pro Met Ala Tyr Ser Phe Pro Val
 870 875 880
 1296 AAT AGG AGA GCC CGC CGT TAT GCC CAG ATT GGG AAA GTT TGC GTG GAG
 Asn Arg Arg Ala Arg Arg Tyr Ala Gln Ile Gly Lys Val Cys Val Glu
 885 890 895
 1344 AAC TGC CAG GAG TTC AGC GGT GTC TCC ATC CAG TAC AAG CTG CAG CCC
 Asn Cys Gln Glu Phe Ser Gly Val Ser Ile Gln Tyr Lys Leu Gln Pro
 900 905 910
 1392 TCC AGC ACC AAC TGC AGT GCC CTA GGT GTG GTC ACC TCA ACA GAA GAC
 Ser Ser Thr Asn Cys Ser Ala Leu Gly Val Val Thr Ser Thr Glu Asp
 915 920 925
 1440 ACC TCA GGG ACC CTA TAT GTA AAT GAC ACG GAG GCC CTG CGG CGA CCT

Thr Ser Gly Thr Leu Tyr Val Asn Asp Thr Glu Ala Leu Arg Arg Pro
 930 935 940 945
 1488 GAG TGT ACC GAG CTT CAG TAC ACA GTG GTA GCC ACT GAC CGG CAG ACC
 Glu Cys Thr Glu Leu Gln Tyr Thr Val Val Ala Thr Asp Arg Gln Thr
 950 955 960
 1536 CGC AGG CAG ACC CAA GCT TCG TTA GTC GTC ACA GTG GAG GGG ACA TAC
 Arg Arg Gln Thr Gln Ala Ser Leu Val Val Thr Val Glu Gly Thr Tyr
 965 970 975
 1584 ATT GCA GAA GAA GTG GGC TGC CCC AAG TCC TGT GCA GTA AAC AAG AGG
 Ile Ala Glu Glu Val Gly Cys Pro Lys Ser Cys Ala Val Asn Lys Arg
 980 985 990
 1632 CGA CCT GAG TGT GAG GAG TGT GGT GGC CTG GGT TCT CCA ACT GGC AGA
 Arg Pro Glu Cys Glu Glu Cys Gly Gly Leu Gly Ser Pro Thr Gly Arg
 995 1000 1005
 1680 TGT GAG TGG CGT CAG GGA GAT GGT AAA GGG ATC ACC AGG AAC TTC TCC
 Cys Glu Trp Arg Gln Gly Asp Gly Lys Gly Ile Thr Arg Asn Phe Ser
 1010 1015 1020 1025
 1728 ACC TGT TCT CCT AGC ACC AGG ACC TGT CCT GAT GGC CAC TGT GAT GCT
 Thr Cys Ser Pro Ser Thr Arg Thr Cys Pro Asp Gly His Cys Asp Ala
 1030 1035 1040
 1776 CTG GAG AGC CGG GAT ATC AAC ATT TGC CCC CAG GAC TGT CTC CGT GGC
 Leu Glu Ser Arg Asp Ile Asn Ile Cys Pro Gln Asp Cys Leu Arg Gly
 1045 1050 1055
 1824 CCC ATT GTT GGC GGG CAT GAG CGA GGG GAG CGC CAG GGG ATT AAA GCC
 Pro Ile Val Gly Gly His Glu Arg Gly Glu Arg Gln Gly Ile Lys Ala
 1060 1065 1070
 1872 GGC TAT GGC ATC TGC AAC TGT TTC CCT GAT GAG AAG AAG TGC TTC TGC
 Gly Tyr Gly Ile Cys Asn Cys Phe Pro Asp Glu Lys Lys Cys Phe Cys
 1075 1080 1085
 1920 GAG CCA GAG GAC AGC CAG GGC CCA TTG TGT GAT GCG CTG TGC CGC ACG
 Glu Pro Glu Asp Ser Gln Gly Pro Leu Cys Asp Ala Leu Cys Arg Thr
 1090 1095 1100 1105
 1926 GTCGAC

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 637 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Met Ala Lys Ala Thr Ser Gly Ala Ala Gly Leu Gly Leu Lys Leu Phe
1 5 10 15
Leu Leu Leu Pro Leu Leu Gly Glu Ala Pro Leu Gly Leu Tyr Phe Ser
20 25 30
Arg Asp Ala Tyr Trp Glu Arg Leu Tyr Val Asp Gln Pro Ala Gly Thr
35 40 45
Pro Leu Leu Tyr Val His Ala Leu Arg Asp Ala Pro Gly Glu Val Pro
50 55 60
Ser Phe Arg Leu Gly Gln Tyr Leu Tyr Gly Val Tyr Arg Thr Arg Leu
65 70 75 80
His Glu Asn Asp Trp Ile His Ile Asp Ala Gly Thr Gly Leu Leu Tyr
85 90 95
Leu Asn Gln Ser Leu Asp His Ser Ser Trp Glu Gln Leu Ser Ile Arg
100 105 110
Asn Gly Gly Phe Pro Leu Leu Thr Val Phe Leu Gln Val Phe Leu Gly
115 120 125
Ser Thr Ala Gln Arg Glu Gly Glu Cys His Trp Pro Gly Cys Ala Arg
130 135 140
Val Tyr Phe Ser Phe Ile Asn Asp Thr Phe Pro Asn Cys Ser Ser Phe
145 150 155 160
Lys Ala Arg Asp Leu Cys Thr Pro Glu Thr Gly Val Ser Phe Arg Ile
165 170 175
Arg Glu Asn Arg Pro Pro Gly Thr Phe Tyr Gln Phe Arg Met Leu Pro
180 185 190
Val Gln Phe Leu Cys Pro Asn Ile Ser Val Lys Tyr Lys Leu Leu Glu
195 200 205
Gly Asp Gly Leu Pro Phe Arg Cys Asp Pro Asp Cys Leu Glu Val Ser
210 215 220
Thr Arg Trp Ala Leu Asp Arg Glu Leu Gln Glu Lys Tyr Val Leu Glu
225 230 235 240
Ala Glu Cys Ala Val Ala Gly Pro Gly Ala Asn Lys Glu Lys Val Ala
245 250 255
Val Ser Phe Pro Val Thr Val Tyr Asp Glu Asp Asp Ser Pro Pro Thr
260 265 270
Phe Ser Gly Gly Val Gly Thr Ala Ser Ala Val Val Glu Phe Lys Arg
275 280 285
Lys Glu Gly Thr Val Val Ala Thr Leu Gln Val Phe Asp Ala Asp Val
290 295 300
Val Pro Ala Ser Gly Glu Leu Val Arg Arg Tyr Thr Ser Thr Leu Leu
305 310 315 320
Ser Gly Asp Ser Trp Ala Gln Gln Thr Phe Arg Val Glu His Thr Pro
325 330 335

Asn Glu Thr Leu Val Gln Ser Asn Asn Asn Ser Val Arg Ala Thr Met
 340 345 350
 His Asn Tyr Lys Leu Val Leu Asn Arg Ser Leu Ser Ile Ser Glu Ser
 355 360 365
 Arg Val Leu Gln Leu Val Val Leu Val Asn Asp Ser Asp Phe Gln Gly
 370 375 380
 Pro Gly Ser Gly Val Leu Phe Leu His Phe Asn Val Ser Val Leu Pro
 385 390 395 400
 Val Thr Leu Asn Leu Pro Met Ala Tyr Ser Phe Pro Val Asn Arg Arg
 405 410 415
 Ala Arg Arg Tyr Ala Gln Ile Gly Lys Val Cys Val Glu Asn Cys Gln
 420 425 430
 Glu Phe Ser Gly Val Ser Ile Gln Tyr Lys Leu Gln Pro Ser Ser Thr
 435 440 445
 Asn Cys Ser Ala Leu Gly Val Val Thr Ser Thr Glu Asp Thr Ser Gly
 450 455 460
 Thr Leu Tyr Val Asn Asp Thr Glu Ala Leu Arg Arg Pro Glu Cys Thr
 465 470 475 480
 Glu Leu Gln Tyr Thr Val Val Ala Thr Asp Arg Gln Thr Arg Arg Gln
 485 490 495
 Thr Gln Ala Ser Leu Val Val Thr Val Glu Gly Thr Tyr Ile Ala Glu
 500 505 510
 Glu Val Gly Cys Pro Lys Ser Cys Ala Val Asn Lys Arg Arg Pro Glu
 515 520 525
 Cys Glu Glu Cys Gly Gly Leu Gly Ser Pro Thr Gly Arg Cys Glu Trp
 530 535 540
 Arg Gln Gly Asp Gly Lys Gly Ile Thr Arg Asn Phe Ser Thr Cys Ser
 545 550 555 560
 Pro Ser Thr Arg Thr Cys Pro Asp Gly His Cys Asp Ala Leu Glu Ser
 565 570 575
 Arg Asp Ile Asn Ile Cys Pro Gln Asp Cys Leu Arg Gly Pro Ile Val
 580 585 590
 Gly Gly His Glu Arg Gly Glu Arg Gln Gly Ile Lys Ala Gly Tyr Gly
 595 600 605
 Ile Cys Asn Cys Phe Pro Asp Glu Lys Lys Cys Phe Cys Glu Pro Glu
 610 615 620
 Asp Ser Gln Gly Pro Leu Cys Asp Ala Leu Cys Arg Thr
 625 630 635

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1223 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..1038

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

```
48  CTG CTG GAG GAT TCC CCA TAT GAA CCA GTT AAC AGC AGA TTG TCA GAT
    Leu Leu Glu Asp Ser Pro Tyr Glu Pro Val Asn Ser Arg Leu Ser Asp
        640                645                650
96  ATA TTC CGG GTG GTC CCA TTC ATA TCA GTG GAG CAC ATT CCC AAA GGG
    Ile Phe Arg Val Val Pro Phe Ile Ser Val Glu His Ile Pro Lys Gly
        655                660                665
144 AAC AAC TGC CTG GAT GCA GCG AAG GCC TGC AAC CTC GAC GAC ATT TGC
    Asn Asn Cys Leu Asp Ala Ala Lys Ala Cys Asn Leu Asp Asp Ile Cys
        670                675                680                685
192 AAG AAG TAC AGG TCG GCG TAC ATC ACC CCG TGC ACC ACC AGC GTG TCC
    Lys Lys Tyr Arg Ser Ala Tyr Ile Thr Pro Cys Thr Thr Ser Val Ser
        690                695                700
240 AAC GAT GTC TGC AAC CGC CGC AAG TGC CAC AAG GCC CTC CGG CAG TTC
    Asn Asp Val Cys Asn Arg Arg Lys Cys His Lys Ala Leu Arg Gln Phe
        705                710                715
288 TTT GAC AAG GTC CCG GCC AAG CAC AGC TAC GGA ATG CTC TTC TGC TCC
    Phe Asp Lys Val Pro Ala Lys His Ser Tyr Gly Met Leu Phe Cys Ser
        720                725                730
336 TGC CGG GAC ATC GCC TGC ACA GAG CGG AGG CGA CAG ACC ATC GTG CCT
    Cys Arg Asp Ile Ala Cys Thr Glu Arg Arg Arg Gln Thr Ile Val Pro
        735                740                745
384 GTG TGC TCC TAT GAA GAG AGG GAG AAG CCC AAC TGT TTG AAT TTG CAG
    Val Cys Ser Tyr Glu Glu Arg Glu Lys Pro Asn Cys Leu Asn Leu Gln
        750                755                760                765
432 GAC TCC TGC AAG ACG AAT TAC ATC TGC AGA TCT CGC CTT GCG GAT TTT
    Asp Ser Cys Lys Thr Asn Tyr Ile Cys Arg Ser Arg Leu Ala Asp Phe
        770                775                780
480 TTT ACC AAC TGC CAG CCA GAG TCA AGG TCT GTC AGC AGC TGT CTA AAG
    Phe Thr Asn Cys Gln Pro Glu Ser Arg Ser Val Ser Ser Cys Leu Lys
        785                790                795
528 GAA AAC TAC GCT GAC TGC CTC CTC GCC TAC TCG GGG CTT ATT GGC ACA
    Glu Asn Tyr Ala Asp Cys Leu Leu Ala Tyr Ser Gly Leu Ile Gly Thr
        800                805                810
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576 GTC ATG ACC CCC AAC TAC ATA GAC TCC AGT AGC CTC AGT GTG GCC CCA
 Val Met Thr Pro Asn Tyr Ile Asp Ser Ser Ser Leu Ser Val Ala Pro
 815 820 825
 624 TGG TGT GAC TGC AGC AAC AGT GGG AAC GAC CTA GAA GAG TGC TTG AAA
 Trp Cys Asp Cys Ser Asn Ser Gly Asn Asp Leu Glu Glu Cys Leu Lys
 830 835 840 845
 672 TTT TTG AAT TTC TTC AAG GAC AAT ACA TGT CTT AAA AAT GCA ATT CAA
 Phe Leu Asn Phe Phe Lys Asp Asn Thr Cys Leu Lys Asn Ala Ile Gln
 850 855 860
 720 GCC TTT GGC AAT GGC TCC GAT GTG ACC GTG TGG CAG CCA GCC TTC CCA
 Ala Phe Gly Asn Gly Ser Asp Val Thr Val Trp Gln Pro Ala Phe Pro
 865 870 875
 768 GTA CAG ACC ACC ACT GCC ACT ACC ACC ACT GCC CTC CGG GTT AAG AAC
 Val Gln Thr Thr Thr Ala Thr Thr Thr Thr Ala Leu Arg Val Lys Asn
 880 885 890
 816 AAG CCC CTG GGG CCA GCA GGG TCT GAG AAT GAA ATT CCC ACT CAT GTT
 Lys Pro Leu Gly Pro Ala Gly Ser Glu Asn Glu Ile Pro Thr His Val
 895 900 905
 864 TTG CCA CCG TGT GCA AAT TTA CAG GCA CAG AAG CTG AAA TCC AAT GTG
 Leu Pro Pro Cys Ala Asn Leu Gln Ala Gln Lys Leu Lys Ser Asn Val
 910 915 920 925
 912 TCG GGC AAT ACA CAC CTC TGT ATT TCC AAT GGT AAT TAT GAA AAA GAA
 Ser Gly Asn Thr His Leu Cys Ile Ser Asn Gly Asn Tyr Glu Lys Glu
 930 935 940
 960 GGT CTC GGT GCT TCC AGC CAC ATA ACC ACA AAA TCA ATG GCT GCT CCT
 Gly Leu Gly Ala Ser Ser His Ile Thr Thr Lys Ser Met Ala Ala Pro
 945 950 955
 1008 CCA AGC TGT GGT CTG AGC CCA CTG CTG GTC CTG GTG GTA ACC GCT CTG
 Pro Ser Cys Gly Leu Ser Pro Leu Leu Val Leu Val Val Thr Ala Leu
 960 965 970
 1058 TCC ACC CTA TTA TCT TTA ACA GAA ACA TCA TAGCTGCATT AAAAAAATAC
 Ser Thr Leu Leu Ser Leu Thr Glu Thr Ser
 975 980
 1118 AATATGGACA TGTA AAAAGA CAAAAACCAA GTTATCTGTT TCCTGTTCTC TTGTATAGCT
 1178 GAAATTCCAG TTTAGGAGCT CAGTTGAGAA ACAGTTCCAT TCAACTGGAA CATTTTTTTT
 1223 TTTTCCTTTT AAGAAAGCTT CTTGTGATCC TTCGGGGCTT CTGTG

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 346 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Leu Leu Glu Asp Ser Pro Tyr Glu Pro Val Asn Ser Arg Leu Ser Asp
1 5 10 15
Ile Phe Arg Val Val Pro Phe Ile Ser Val Glu His Ile Pro Lys Gly
20 25 30
Asn Asn Cys Leu Asp Ala Ala Lys Ala Cys Asn Leu Asp Asp Ile Cys
35 40 45
Lys Lys Tyr Arg Ser Ala Tyr Ile Thr Pro Cys Thr Thr Ser Val Ser
50 55 60
Asn Asp Val Cys Asn Arg Arg Lys Cys His Lys Ala Leu Arg Gln Phe
65 70 75 80
Phe Asp Lys Val Pro Ala Lys His Ser Tyr Gly Met Leu Phe Cys Ser
85 90 95
Cys Arg Asp Ile Ala Cys Thr Glu Arg Arg Arg Gln Thr Ile Val Pro
100 105 110
Val Cys Ser Tyr Glu Glu Arg Glu Lys Pro Asn Cys Leu Asn Leu Gln
115 120 125
Asp Ser Cys Lys Thr Asn Tyr Ile Cys Arg Ser Arg Leu Ala Asp Phe
130 135 140
Phe Thr Asn Cys Gln Pro Glu Ser Arg Ser Val Ser Ser Cys Leu Lys
145 150 155 160
Glu Asn Tyr Ala Asp Cys Leu Leu Ala Tyr Ser Gly Leu Ile Gly Thr
165 170 175
Val Met Thr Pro Asn Tyr Ile Asp Ser Ser Ser Leu Ser Val Ala Pro
180 185 190
Trp Cys Asp Cys Ser Asn Ser Gly Asn Asp Leu Glu Glu Cys Leu Lys
195 200 205
Phe Leu Asn Phe Phe Lys Asp Asn Thr Cys Leu Lys Asn Ala Ile Gln
210 215 220
Ala Phe Gly Asn Gly Ser Asp Val Thr Val Trp Gln Pro Ala Phe Pro
225 230 235 240
Val Gln Thr Thr Thr Ala Thr Thr Thr Thr Ala Leu Arg Val Lys Asn
245 250 255
Lys Pro Leu Gly Pro Ala Gly Ser Glu Asn Glu Ile Pro Thr His Val
260 265 270
Leu Pro Pro Cys Ala Asn Leu Gln Ala Gln Lys Leu Lys Ser Asn Val
275 280 285

Ser Gly Asn Thr His Leu Cys Ile Ser Asn Gly Asn Tyr Glu Lys Glu
 290 295 300

Gly Leu Gly Ala Ser Ser His Ile Thr Thr Lys Ser Met Ala Ala Pro
 305 310 315 320

Pro Ser Cys Gly Leu Ser Pro Leu Leu Val Leu Val Val Thr Ala Leu
 325 330 335

Ser Thr Leu Leu Ser Leu Thr Glu Thr Ser
 340 345

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1682 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 118..1497

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

60 GGGCGGCCAG AGCAGCACAG CTGTCCGGGG ATCGCTGCAT GCTGAGCTCC CTCGGCAAGA

117 CCCAGCGGCG GCTCGGGATT TTTTGGGGG GCGGGGACC AGCCCCGCGC CGGCACC

165 ATG TTC CTG GCG ACC CTG TAC TTC GCG CTG CCG CTC TTG GAC TTG CTC
 Met Phe Leu Ala Thr Leu Tyr Phe Ala Leu Pro Leu Leu Asp Leu Leu
 350 355 360

213 CTG TCG GCC GAA GTG AGC GGC GGA GAC CGC CTG GAT TGC GTG AAA GCC
 Leu Ser Ala Glu Val Ser Gly Gly Asp Arg Leu Asp Cys Val Lys Ala
 365 370 375

261 AGT GAT CAG TGC CTG AAG GAG CAG AGC TGC AGC ACC AAG TAC CGC ACG
 Ser Asp Gln Cys Leu Lys Glu Gln Ser Cys Ser Thr Lys Tyr Arg Thr
 380 385 390

309 CTA AGG CAG TGC GTG GCG GGC AAG GAG ACC AAC TTC AGC CTG GCA TCC
 Leu Arg Gln Cys Val Ala Gly Lys Glu Thr Asn Phe Ser Leu Ala Ser
 395 400 405 410

357 GGC CTG GAG GCC AAG GAT GAG TGC CGC AGC GCC ATG GAG GCC CTG AAG
 Gly Leu Glu Ala Lys Asp Glu Cys Arg Ser Ala Met Glu Ala Leu Lys
 415 420 425

405 CAG AAG TCG CTC TAC AAC TGC CGC TGC AAG CGG GGT ATG AAG AAG GAG
 Gln Lys Ser Leu Tyr Asn Cys Arg Cys Lys Arg Gly Met Lys Lys Glu

	430	435	440
453	AAG AAC TGC CTG CGC ATT TAC	TGG AGC ATG TAC CAG AGC CTG CAG GGA	
	Lys Asn Cys Leu Arg Ile Tyr Trp Ser Met Tyr Gln Ser Leu Gln Gly		
	445	450	455
501	AAT GAT CTG CTG GAG GAT TCC CCA TAT GAA CCA GTT AAC AGC AGA TTG		
	Asn Asp Leu Leu Glu Asp Ser Pro Tyr Glu Pro Val Asn Ser Arg Leu		
	460	465	470
549	TCA GAT ATA TTC CGG GTG GTC CCA TTC ATA TCA GTG GAG CAC ATT CCC		
	Ser Asp Ile Phe Arg Val Val Pro Phe Ile Ser Val Glu His Ile Pro		
	475	480	485 490
597	AAA GGG AAC AAC TGC CTG GAT GCA GCG AAG GCC TGC AAC CTC GAC GAC		
	Lys Gly Asn Asn Cys Leu Asp Ala Ala Lys Ala Cys Asn Leu Asp Asp		
	495	500	505
645	ATT TGC AAG AAG TAC AGG TCG GCG TAC ATC ACC CCG TGC ACC ACC AGC		
	Ile Cys Lys Lys Tyr Arg Ser Ala Tyr Ile Thr Pro Cys Thr Thr Ser		
	510	515	520
693	GTG TCC AAC GAT GTC TGC AAC CGC CGC AAG TGC CAC AAG GCC CTC CGG		
	Val Ser Asn Asp Val Cys Asn Arg Arg Lys Cys His Lys Ala Leu Arg		
	525	530	535
741	CAG TTC TTT GAC AAG GTC CCG GCC AAG CAC AGC TAC GGA ATG CTC TTC		
	Gln Phe Phe Asp Lys Val Pro Ala Lys His Ser Tyr Gly Met Leu Phe		
	540	545	550
789	TGC TCC TGC CGG GAC ATC GCC TGC ACA GAG CGG AGG CGA CAG ACC ATC		
	Cys Ser Cys Arg Asp Ile Ala Cys Thr Glu Arg Arg Arg Gln Thr Ile		
	555	560	565 570
837	GTG CCT GTG TGC TCC TAT GAA GAG AGG GAG AAG CCC AAC TGT TTG AAT		
	Val Pro Val Cys Ser Tyr Glu Glu Arg Glu Lys Pro Asn Cys Leu Asn		
	575	580	585
885	TTG CAG GAC TCC TGC AAG ACG AAT TAC ATC TGC AGA TCT CGC CTT GCG		
	Leu Gln Asp Ser Cys Lys Thr Asn Tyr Ile Cys Arg Ser Arg Leu Ala		
	590	595	600
933	GAT TTT TTT ACC AAC TGC CAG CCA GAG TCA AGG TCT GTC AGC AGC TGT		
	Asp Phe Phe Thr Asn Cys Gln Pro Glu Ser Arg Ser Val Ser Ser Cys		
	605	610	615
981	CTA AAG GAA AAC TAC GCT GAC TGC CTC CTC GCC TAC TCG GGG CTT ATT		
	Leu Lys Glu Asn Tyr Ala Asp Cys Leu Leu Ala Tyr Ser Gly Leu Ile		
	620	625	630
1029	GGC ACA GTC ATG ACC CCC AAC TAC ATA GAC TCC AGT AGC CTC AGT GTG		
	Gly Thr Val Met Thr Pro Asn Tyr Ile Asp Ser Ser Ser Leu Ser Val		

635	640	645	650
1077	GCC CCA TGG TGT GAC TGC AGC AAC AGT GGG AAC GAC CTA GAA GAG TGC		
	Ala Pro Trp Cys Asp Cys Ser Asn Ser Gly Asn Asp Leu Glu Glu Cys	660	665
1125	TTG AAA TTT TTG AAT TTC TTC AAG GAC AAT ACA TGT CTT AAA AAT GCA		
	Leu Lys Phe Leu Asn Phe Phe Lys Asp Asn Thr Cys Leu Lys Asn Ala	670	680
1173	ATT CAA GCC TTT GGC AAT GGC TCC GAT GTG ACC GTG TGG CAG CCA GCC		
	Ile Gln Ala Phe Gly Asn Gly Ser Asp Val Thr Val Trp Gln Pro Ala	685	695
1221	TTC CCA GTA CAG ACC ACC ACT GCC ACT ACC ACC ACT GCC CTC CGG GTT		
	Phe Pro Val Gln Thr Thr Thr Ala Thr Thr Thr Thr Ala Leu Arg Val	700	710
1269	AAG AAC AAG CCC CTG GGG CCA GCA GGG TCT GAG AAT GAA ATT CCC ACT		
	Lys Asn Lys Pro Leu Gly Pro Ala Gly Ser Glu Asn Glu Ile Pro Thr	715	730
1317	CAT GTT TTG CCA CCG TGT GCA AAT TTA CAG GCA CAG AAG CTG AAA TCC		
	His Val Leu Pro Pro Cys Ala Asn Leu Gln Ala Gln Lys Leu Lys Ser	735	745
1365	AAT GTG TCG GGC AAT ACA CAC CTC TGT ATT TCC AAT GGT AAT TAT GAA		
	Asn Val Ser Gly Asn Thr His Leu Cys Ile Ser Asn Gly Asn Tyr Glu	750	760
1413	AAA GAA GGT CTC GGT GCT TCC AGC CAC ATA ACC ACA AAA TCA ATG GCT		
	Lys Glu Gly Leu Gly Ala Ser Ser His Ile Thr Thr Lys Ser Met Ala	765	775
1461	GCT CCT CCA AGC TGT GGT CTG AGC CCA CTG CTG GTC CTG GTG GTA ACC		
	Ala Pro Pro Ser Cys Gly Leu Ser Pro Leu Leu Val Leu Val Val Thr	780	790
1507	GCT CTG TCC ACC CTA TTA TCT TTA ACA GAA ACA TCA TAGCTGCATT		
	Ala Leu Ser Thr Leu Leu Ser Leu Thr Glu Thr Ser	795	805
1567	AAAAAAATAC AATATGGACA TGTA AAAAGA CAAAAACCAA GTTATCTGTT TCCTGTCTC		
1627	TTGTATAGCT GAAATTCAG TTTAGGAGCT CAGTTGAGAA ACAGTCCAT TCAACTGGAA		
1682	CATTTTTTTT TTTTCCTTTT AAGAAAGCTT CTTGTGATCC TTCGGGGCTT CTGTG		

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 460 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

```

Met Phe Leu Ala Thr Leu Tyr Phe Ala Leu Pro Leu Leu Asp Leu Leu
 1           5           10           15
Leu Ser Ala Glu Val Ser Gly Gly Asp Arg Leu Asp Cys Val Lys Ala
          20           25           30
Ser Asp Gln Cys Leu Lys Glu Gln Ser Cys Ser Thr Lys Tyr Arg Thr
          35           40           45
Leu Arg Gln Cys Val Ala Gly Lys Glu Thr Asn Phe Ser Leu Ala Ser
          50           55           60
Gly Leu Glu Ala Lys Asp Glu Cys Arg Ser Ala Met Glu Ala Leu Lys
          65           70           75           80
Gln Lys Ser Leu Tyr Asn Cys Arg Cys Lys Arg Gly Met Lys Lys Glu
          85           90           95
Lys Asn Cys Leu Arg Ile Tyr Trp Ser Met Tyr Gln Ser Leu Gln Gly
          100          105          110
Asn Asp Leu Leu Glu Asp Ser Pro Tyr Glu Pro Val Asn Ser Arg Leu
          115          120          125
Ser Asp Ile Phe Arg Val Val Pro Phe Ile Ser Val Glu His Ile Pro
          130          135          140
Lys Gly Asn Asn Cys Leu Asp Ala Ala Lys Ala Cys Asn Leu Asp Asp
          145          150          155          160
Ile Cys Lys Lys Tyr Arg Ser Ala Tyr Ile Thr Pro Cys Thr Thr Ser
          165          170          175
Val Ser Asn Asp Val Cys Asn Arg Arg Lys Cys His Lys Ala Leu Arg
          180          185          190
Gln Phe Phe Asp Lys Val Pro Ala Lys His Ser Tyr Gly Met Leu Phe
          195          200          205
Cys Ser Cys Arg Asp Ile Ala Cys Thr Glu Arg Arg Arg Gln Thr Ile
          210          215          220
Val Pro Val Cys Ser Tyr Glu Glu Arg Glu Lys Pro Asn Cys Leu Asn
          225          230          235          240
Leu Gln Asp Ser Cys Lys Thr Asn Tyr Ile Cys Arg Ser Arg Leu Ala
          245          250          255
Asp Phe Phe Thr Asn Cys Gln Pro Glu Ser Arg Ser Val Ser Ser Cys
          260          265          270
Leu Lys Glu Asn Tyr Ala Asp Cys Leu Leu Ala Tyr Ser Gly Leu Ile
          275          280          285
Gly Thr Val Met Thr Pro Asn Tyr Ile Asp Ser Ser Ser Leu Ser Val
          290          295          300

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Ala Pro Trp Cys Asp Cys Ser Asn Ser Gly Asn Asp Leu Glu Glu Cys
 305 310 315 320

Leu Lys Phe Leu Asn Phe Phe Lys Asp Asn Thr Cys Leu Lys Asn Ala
 325 330 335

Ile Gln Ala Phe Gly Asn Gly Ser Asp Val Thr Val Trp Gln Pro Ala
 340 345 350

Phe Pro Val Gln Thr Thr Thr Ala Thr Thr Thr Thr Ala Leu Arg Val
 355 360 365

Lys Asn Lys Pro Leu Gly Pro Ala Gly Ser Glu Asn Glu Ile Pro Thr
 370 375 380

His Val Leu Pro Pro Cys Ala Asn Leu Gln Ala Gln Lys Leu Lys Ser
 385 390 395 400

Asn Val Ser Gly Asn Thr His Leu Cys Ile Ser Asn Gly Asn Tyr Glu
 405 410 415

Lys Glu Gly Leu Gly Ala Ser Ser His Ile Thr Thr Lys Ser Met Ala
 420 425 430

Ala Pro Pro Ser Cys Gly Leu Ser Pro Leu Leu Val Leu Val Val Thr
 435 440 445

Ala Leu Ser Thr Leu Leu Ser Leu Thr Glu Thr Ser
 450 455 460

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1888 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 25..1416

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

51 AAAAAACGGT GGGATTTATT TAAC ATG ATC TTG GCA AAC GTC TTC TGC CTC
 Met Ile Leu Ala Asn Val Phe Cys Leu
 465

99 TTC TTC TTT CTA GAC GAG ACC CTC CGC TCT TTG GCC AGC CCT TCC TCC
 Phe Phe Phe Leu Asp Glu Thr Leu Arg Ser Leu Ala Ser Pro Ser Ser
 470 475 480 485

147 CTG CAG GGC CCC GAG CTC CAC GGC TGG CGC CCC CCA GTG GAC TGT GTC
 Leu Gln Gly Pro Glu Leu His Gly Trp Arg Pro Pro Val Asp Cys Val
 490 495 500

195 CGG GCC AAT GAG CTG TGT GCC GCC GAA TCC AAC TGC AGC TCT CGC TAC

Arg Ala Asn Glu Leu Cys Ala Ala Glu Ser Asn Cys Ser Ser Arg Tyr
 505 510 515
 243 CGC ACT CTG CGG CAG TGC CTG GCA GGC CGC GAC CGC AAC ACC ATG CTG
 Arg Thr Leu Arg Gln Cys Leu Ala Gly Arg Asp Arg Asn Thr Met Leu
 520 525 530
 291 GCC AAC AAG GAG TGC CAG GCG GCC TTG GAG GTC TTG CAG GAG AGC CCG
 Ala Asn Lys Glu Cys Gln Ala Ala Leu Glu Val Leu Gln Glu Ser Pro
 535 540 545
 339 CTG TAC GAC TGC CGC TGC AAG CGG GGC ATG AAG AAG GAG CTG CAG TGT
 Leu Tyr Asp Cys Arg Cys Lys Arg Gly Met Lys Lys Glu Leu Gln Cys
 550 555 560 565
 387 CTG CAG ATC TAC TGG AGC ATC CAC CTG GGG CTG ACC GAG GGT GAG GAG
 Leu Gln Ile Tyr Trp Ser Ile His Leu Gly Leu Thr Glu Gly Glu Glu
 570 575 580
 435 TTC TAC GAA GCC TCC CCC TAT GAG CCG GTG ACC TCC CGC CTC TCG GAC
 Phe Tyr Glu Ala Ser Pro Tyr Glu Pro Val Thr Ser Arg Leu Ser Asp
 585 590 595
 483 ATC TTC AGG CTT GCT TCA ATC TTC TCA GGG ACA GGG GCA GAC CCG GTG
 Ile Phe Arg Leu Ala Ser Ile Phe Ser Gly Thr Gly Ala Asp Pro Val
 600 605 610
 531 GTC AGC GCC AAG AGC AAC CAT TGC CTG GAT GCT GCC AAG GCC TGC AAC
 Val Ser Ala Lys Ser Asn His Cys Leu Asp Ala Ala Lys Ala Cys Asn
 615 620 625
 579 CTG AAT GAC AAC TGC AAG AAG CTG CGC TCC TCC TAC ATC TCC ATC TGC
 Leu Asn Asp Asn Cys Lys Lys Leu Arg Ser Ser Tyr Ile Ser Ile Cys
 630 635 640 645
 627 AAC CGC GAG ATC TCG CCC ACC GAG CGC TGC AAC CGC CGC AAG TGC CAC
 Asn Arg Glu Ile Ser Pro Thr Glu Arg Cys Asn Arg Arg Lys Cys His
 650 655 660
 675 AAG GCC CTG CGC CAG TTC TTC GAC CGG GTG CCC AGC GAG TAC ACC TAC
 Lys Ala Leu Arg Gln Phe Phe Asp Arg Val Pro Ser Glu Tyr Thr Tyr
 665 670 675
 723 CGC ATG CTC TTC TGC TCC TGC CAA GAC CAG GCG TGC GCT GAG CGC CGC
 Arg Met Leu Phe Cys Ser Cys Gln Asp Gln Ala Cys Ala Glu Arg Arg
 680 685 690
 771 CGG CAA ACC ATC CTG CCC AGC TGC TCC TAT GAG GAC AAG GAG AAG CCC
 Arg Gln Thr Ile Leu Pro Ser Cys Ser Tyr Glu Asp Lys Glu Lys Pro
 695 700 705
 819 AAC TGC CTG GAC CTG CGT GGC GTG TGC CGG ACT GAC CAC CTG TGT CGG

Asn Cys Leu Asp Leu Arg Gly Val Cys Arg Thr Asp His Leu Cys Arg
 710 715 720 725
 867 TCC CGG CTG GCC GAC TTC CAT GCC AAT TGT CGA GCC TCC TAC CAG ACG
 Ser Arg Leu Ala Asp Phe His Ala Asn Cys Arg Ala Ser Tyr Gln Thr
 730 735 740
 915 GTC ACC AGC TGC CCT GCG GAC AAT TAC CAG GCG TGT CTG GGC TCT TAT
 Val Thr Ser Cys Pro Ala Asp Asn Tyr Gln Ala Cys Leu Gly Ser Tyr
 745 750 755
 963 GCT GGC ATG ATT GGG TTT GAC ATG ACA CCT AAC TAT GTG GAC TCC AGC
 Ala Gly Met Ile Gly Phe Asp Met Thr Pro Asn Tyr Val Asp Ser Ser
 760 765 770
 1011 CCC ACT GGC ATC GTG GTG TCC CCC TGG TGC AGC TGT CGT GGC AGC GGG
 Pro Thr Gly Ile Val Val Ser Pro Trp Cys Ser Cys Arg Gly Ser Gly
 775 780 785
 1059 AAC ATG GAG GAG GAG TGT GAG AAG TTC CTC AGG GAC TTC ACC GAG AAC
 Asn Met Glu Glu Glu Cys Glu Lys Phe Leu Arg Asp Phe Thr Glu Asn
 790 795 800 805
 1107 CCA TGC CTC CGG AAC GCC ATC CAG GCC TTT GGC AAC GGC ACG GAC GTG
 Pro Cys Leu Arg Asn Ala Ile Gln Ala Phe Gly Asn Gly Thr Asp Val
 810 815 820
 1155 AAC GTG TCC CCA AAA GGC CCC TCG TTC CAG GCC ACC CAG GCC CCT CGG
 Asn Val Ser Pro Lys Gly Pro Ser Phe Gln Ala Thr Gln Ala Pro Arg
 825 830 835
 1203 GTG GAG AAG ACG CCT TCT TTG CCA GAT GAC CTC AGT GAC AGT ACC AGC
 Val Glu Lys Thr Pro Ser Leu Pro Asp Asp Leu Ser Asp Ser Thr Ser
 840 845 850
 1251 TTG GGG ACC AGT GTC ATC ACC ACC TGC ACG TCT GTC CAG GAG CAG GGG
 Leu Gly Thr Ser Val Ile Thr Thr Cys Thr Ser Val Gln Glu Gln Gly
 855 860 865
 1299 CTG AAG GCC AAC AAC TCC AAA GAG TTA AGC ATG TGC TTC ACA GAG CTC
 Leu Lys Ala Asn Asn Ser Lys Glu Leu Ser Met Cys Phe Thr Glu Leu
 870 875 880 885
 1347 ACG ACA AAT ATC ATC CCA GGG AGT AAC AAG GTG ATC AAA CCT AAC TCA
 Thr Thr Asn Ile Ile Pro Gly Ser Asn Lys Val Ile Lys Pro Asn Ser
 890 895 900
 1395 GGC CCC AGC AGA GCC AGA CCG TCG GCT GCC TTG ACC GTG CTG TCT GTC
 Gly Pro Ser Arg Ala Arg Pro Ser Ala Ala Leu Thr Val Leu Ser Val
 905 910 915
 1446 CTG ATG CTG AAA CTG GCC TTG TAGGCTGTGG GAACCGAGTC AGAAGATTTT

Leu Met Leu Lys Leu Ala Leu
920

1506 TGAAAGCTAC GCAGACAAGA ACAGCCGCCT GACGAAATGG AAACACACAC AGACACACAC
1566 ACACCTTGCA AAAAAAAT TGTMTTCCC ACCTTGTCGC TGAACCTGTC TCCTCCCAGG
1626 TTTCTTCTCT GGAGAAGTTT TTGTAAACCA AACAGACAAG CAGGCAGGCA GCCTGAGAGC
1686 TGGCCCAGGG GTCCCCTGGC AGGGGAAACT CTGGTGCCGG GGAGGGCACG AGGCTCTAGA
1746 AATGCCCTTC ACTTTCTCCT GGTGTTTTTC TCTCTGGACC CTTCTGAAGC AGAGACCGGA
1806 CAAGAGCCTG CAGCGGAAGG GACTCTGGGC TGTGCCTGAG GCTGGCTGGG GGCAGGACAA
1866 CACAGCTGCT TCCCCAGGCT GCCCACTCTG GGGACCCGCT GGGGGCTGGC AGAGGGCATC
1888 GGTCAGCGGG GCAGCGGGGC TG

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 464 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Met	Ile	Leu	Ala	Asn	Val	Phe	Cys	Leu	Phe	Phe	Phe	Leu	Asp	Glu	Thr
1				5				10						15	
Leu	Arg	Ser	Leu	Ala	Ser	Pro	Ser	Ser	Leu	Gln	Gly	Pro	Glu	Leu	His
			20					25						30	
Gly	Trp	Arg	Pro	Pro	Val	Asp	Cys	Val	Arg	Ala	Asn	Glu	Leu	Cys	Ala
			35				40						45		
Ala	Glu	Ser	Asn	Cys	Ser	Ser	Arg	Tyr	Arg	Thr	Leu	Arg	Gln	Cys	Leu
			50			55					60				
Ala	Gly	Arg	Asp	Arg	Asn	Thr	Met	Leu	Ala	Asn	Lys	Glu	Cys	Gln	Ala
			65			70				75					80
Ala	Leu	Glu	Val	Leu	Gln	Glu	Ser	Pro	Leu	Tyr	Asp	Cys	Arg	Cys	Lys
			85						90					95	
Arg	Gly	Met	Lys	Lys	Glu	Leu	Gln	Cys	Leu	Gln	Ile	Tyr	Trp	Ser	Ile
			100					105					110		
His	Leu	Gly	Leu	Thr	Glu	Gly	Glu	Glu	Phe	Tyr	Glu	Ala	Ser	Pro	Tyr
			115				120					125			
Glu	Pro	Val	Thr	Ser	Arg	Leu	Ser	Asp	Ile	Phe	Arg	Leu	Ala	Ser	Ile
			130				135					140			

Phe Ser Gly Thr Gly Ala Asp Pro Val Val Ser Ala Lys Ser Asn His
145 150 155 160
Cys Leu Asp Ala Ala Lys Ala Cys Asn Leu Asn Asp Asn Cys Lys Lys
165 170 175
Leu Arg Ser Ser Tyr Ile Ser Ile Cys Asn Arg Glu Ile Ser Pro Thr
180 185 190
Glu Arg Cys Asn Arg Arg Lys Cys His Lys Ala Leu Arg Gln Phe Phe
195 200 205
Asp Arg Val Pro Ser Glu Tyr Thr Tyr Arg Met Leu Phe Cys Ser Cys
210 215 220
Gln Asp Gln Ala Cys Ala Glu Arg Arg Arg Gln Thr Ile Leu Pro Ser
225 230 235 240
Cys Ser Tyr Glu Asp Lys Glu Lys Pro Asn Cys Leu Asp Leu Arg Gly
245 250 255
Val Cys Arg Thr Asp His Leu Cys Arg Ser Arg Leu Ala Asp Phe His
260 265 270
Ala Asn Cys Arg Ala Ser Tyr Gln Thr Val Thr Ser Cys Pro Ala Asp
275 280 285
Asn Tyr Gln Ala Cys Leu Gly Ser Tyr Ala Gly Met Ile Gly Phe Asp
290 295 300
Met Thr Pro Asn Tyr Val Asp Ser Ser Pro Thr Gly Ile Val Val Ser
305 310 315 320
Pro Trp Cys Ser Cys Arg Gly Ser Gly Asn Met Glu Glu Glu Cys Glu
325 330 335
Lys Phe Leu Arg Asp Phe Thr Glu Asn Pro Cys Leu Arg Asn Ala Ile
340 345 350
Gln Ala Phe Gly Asn Gly Thr Asp Val Asn Val Ser Pro Lys Gly Pro
355 360 365
Ser Phe Gln Ala Thr Gln Ala Pro Arg Val Glu Lys Thr Pro Ser Leu
370 375 380
Pro Asp Asp Leu Ser Asp Ser Thr Ser Leu Gly Thr Ser Val Ile Thr
385 390 395 400
Thr Cys Thr Ser Val Gln Glu Gln Gly Leu Lys Ala Asn Asn Ser Lys
405 410 415
Glu Leu Ser Met Cys Phe Thr Glu Leu Thr Thr Asn Ile Ile Pro Gly
420 425 430
Ser Asn Lys Val Ile Lys Pro Asn Ser Gly Pro Ser Arg Ala Arg Pro
435 440 445
Ser Ala Ala Leu Thr Val Leu Ser Val Leu Met Leu Lys Leu Ala Leu
450 455 460

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

60 CGCGGCGCCC AGCGCAGGCA GAGCGCTGTC GCATCCC GGG CGTCCACCCG CCATGGGGCT

120 CTCCTGGAGC CCGCGACCTC CACTGCTGAT GATCCTGCTA CTGGTGCTGT CGTTGTGGCT

180 GCCACTTGGA GCAGGAAACT CCCTTGCCAC AGAGAACAGG TTTGTGAACA GCTGTACCCA

231 GGCCAGAAAG AAATGCGAGG CTAA TCC CGC TTG CAA GGC TGC CTA CCA GCA

Ser Arg Leu Gln Gly Cys Leu Pro Ala
465 470

279 CCT GGG CTC CTG CAC CTC CAG TTA AGC AGG CCG CTG CCC TTA GAG GAG

Pro Gly Leu Leu His Leu Gln Leu Ser Arg Pro Leu Pro Leu Glu Glu
475 480 485

327 TCT GCC ATG TCT GCA GAC TGC CTA GAG GCA GCA GAA CAA CTC AGG AAC

Ser Ala Met Ser Ala Asp Cys Leu Glu Ala Ala Glu Gln Leu Arg Asn
490 495 500 505

375 AGC TCT CTG ATA GAC TGC AGG TGC CAT CGG CGC ATG AAG CAC CAA GCT

Ser Ser Leu Ile Asp Cys Arg Cys His Arg Arg Met Lys His Gln Ala
510 515 520

423 ACC TGT CTG GAC ATT TAT TGG ACC GTT CAC CCT GCC CGA AGC CTT GGT

Thr Cys Leu Asp Ile Tyr Trp Thr Val His Pro Ala Arg Ser Leu Gly
525 530 535

471 GAC TAC GAG TTG GAT GTC TCA CCC TAT GAA GAC ACA GTG ACC AGC AAA

Asp Tyr Glu Leu Asp Val Ser Pro Tyr Glu Asp Thr Val Thr Ser Lys
540 545 550

519 CCC TGG AAA ATG AAT CTT AGC AAG TTG AAC ATG CTC AAA CCA GAC TCG

Pro Trp Lys Met Asn Leu Ser Lys Leu Asn Met Leu Lys Pro Asp Ser
555 560 565

567 GAC CTC TGC CTC AAA TTT GCT ATG CTG TGT ACT CTT CAC GAC AAG TGT

Asp Leu Cys Leu Lys Phe Ala Met Leu Cys Thr Leu His Asp Lys Cys
570 575 580 585

615 GAC CGC CTG CGC AAG GCC TAC GGG GAG GCA TGC TCA GGG ATC CGC TGC
 Asp Arg Leu Arg Lys Ala Tyr Gly Glu Ala Cys Ser Gly Ile Arg Cys
 590 595 600

663 CAG CGC CAC CTC TGC CTA GCC CAG CTG CGC TCC TTC TTT GAG AAG GCA
 Gln Arg His Leu Cys Leu Ala Gln Leu Arg Ser Phe Phe Glu Lys Ala
 605 610 615

711 GCA GAG TCC CAC GCT CAG GGT CTG CTG CTG TGT CCC TGT GCA CCA GAA
 Ala Glu Ser His Ala Gln Gly Leu Leu Leu Cys Pro Cys Ala Pro Glu
 620 625 630

759 GAT GCG GGC TGT GGG GAG CGG CGG CGT AAC ACC ATC GCC CCC AGT TGC
 Asp Ala Gly Cys Gly Glu Arg Arg Arg Asn Thr Ile Ala Pro Ser Cys
 635 640 645

807 GCC CTG CCT TCT GTA ACC CCC AAT TGC CTG GAT CTG CGG AGC TTC TGC
 Ala Leu Pro Ser Val Thr Pro Asn Cys Leu Asp Leu Arg Ser Phe Cys
 650 655 660 665

855 CGT GCG GAC CCT TTG TGC AGA TCA CGC CTG ATG GAC TTC CAG ACC CAC
 Arg Ala Asp Pro Leu Cys Arg Ser Arg Leu Met Asp Phe Gln Thr His
 670 675 680

903 TGT CAT CCT ATG GAC ATC CTT GGG ACT TGT GCA ACT GAG CAG TCC AGA
 Cys His Pro Met Asp Ile Leu Gly Thr Cys Ala Thr Glu Gln Ser Arg
 685 690 695

951 TGT CTG CGG GCA TAC CTG GGG CTG ATT GGG ACT GCC ATG ACC CCA AAC
 Cys Leu Arg Ala Tyr Leu Gly Leu Ile Gly Thr Ala Met Thr Pro Asn
 700 705 710

999 TTC ATC AGC AAG GTC AAC ACT ACT GTT GCC TTA AGC TGC ACC TGC CGA
 Phe Ile Ser Lys Val Asn Thr Thr Val Ala Leu Ser Cys Thr Cys Arg
 715 720 725

1047 GGC AGC GGC AAC CTA CAG GAC GAG TGT GAA CAG CTG GAA AGG TCC TTC
 Gly Ser Gly Asn Leu Gln Asp Glu Cys Glu Gln Leu Glu Arg Ser Phe
 730 735 740 745

1095 TCC CAG AAC CCC TGC CTC GTG GAG GCC ATT GCA GCT AAG ATG CGT TTC
 Ser Gln Asn Pro Cys Leu Val Glu Ala Ile Ala Ala Lys Met Arg Phe
 750 755 760

1143 CAC AGA CAG CTC TTC TCC CAG GAC TGG GCA GAC TCT ACT TTT TCA GTG
 His Arg Gln Leu Phe Ser Gln Asp Trp Ala Asp Ser Thr Phe Ser Val
 765 770 775

1191 GTG CAG CAG CAG AAC AGC AAC CCT GCT CTG AGA CTG CAG CCC AGG CTA
 Val Gln Gln Gln Asn Ser Asn Pro Ala Leu Arg Leu Gln Pro Arg Leu
 780 785 790

1239 CCC ATT CTT TCT TTC TCC ATC CTT CCC TTG ATT CTG CTG CAG ACC CTC
 Pro Ile Leu Ser Phe Ser Ile Leu Pro Leu Ile Leu Leu Gln Thr Leu
 795 800 805
 1292 TGG TAGCTGGGCT TCCTCAGGGT CCTTTGTCCT CTCCACCACA CCCAGACTGA
 Trp
 810
 1352 TTTGCAGCCT GTGGTGGGAG AGAACTCGCC AGCCTGTGGA AGAAGACGCA GCGTGCTACA
 CAGCAACCCG GAACCAACCA GGCATTCCGC AGCACATCCC GTCTGCTCCA GAAGAGGTCT
 1412
 1472 TAGAAGTGAG GGCTGTGACC CTTCCGATCC TGAGCGGCTA GTTTTCAAAC CTCCCTTGCC
 CCTGCTTCCT TCTGGCTCAG GCTGCTCCTC CTTAGGACTT TGTGGGTCCA GTTTTGCCTT
 1532
 1592 CTGTTCTGAT GGTGATTAGC GGCTCACCTC CAGCGCTTCT TCCTGTTTCC CAGGACCACC
 CAGAGGCTAA GGAATCAGTC ATTCCCTGTT GCCTTCTCCA GGAAGGCAGG CTAAGGGTTC
 1652
 1712 TGAGGTGACT GAGAAAAATG TTTCTTTTGT GTGGAAGGCT GGTGCTCCAG CCTCCACGTC
 CCTCTGAATG GAAGATAAAA ACCTGCTGGT GTCTTGACTG CTCTGCCAGG CAATCCTGAA
 1772
 1832 CATTTGGGCA TGAAGAGCTA AAGTCTTTGG GTCTTGTTTA ACTCCTATTA CTGTCCCCAA
 1878 ATTCCCCTAG TCCCTTGGGT CATGATTAAA CATTTTGACT TAAAAA

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 346 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Ser	Arg	Leu	Gln	Gly	Cys	Leu	Pro	Ala	Pro	Gly	Leu	Leu	His	Leu	Gln
1				5					10					15	
Leu	Ser	Arg	Pro	Leu	Pro	Leu	Glu	Glu	Ser	Ala	Met	Ser	Ala	Asp	Cys
			20					25					30		
Leu	Glu	Ala	Ala	Glu	Gln	Leu	Arg	Asn	Ser	Ser	Leu	Ile	Asp	Cys	Arg
		35					40					45			
Cys	His	Arg	Arg	Met	Lys	His	Gln	Ala	Thr	Cys	Leu	Asp	Ile	Tyr	Trp
	50					55					60				
Thr	Val	His	Pro	Ala	Arg	Ser	Leu	Gly	Asp	Tyr	Glu	Leu	Asp	Val	Ser

65	70	75	80
Pro Tyr Glu Asp Thr Val Thr Ser Lys	Pro Trp Lys Met Asn Leu Ser		
85	90		95
Lys Leu Asn Met Leu Lys Pro Asp Ser	Asp Leu Cys Leu Lys Phe Ala		
100	105		110
Met Leu Cys Thr Leu His Asp Lys Cys	Asp Arg Leu Arg Lys Ala Tyr		
115	120		125
Gly Glu Ala Cys Ser Gly Ile Arg Cys	Gln Arg His Leu Cys Leu Ala		
130	135		140
Gln Leu Arg Ser Phe Phe Glu Lys Ala	Ala Glu Ser His Ala Gln Gly		
145	150		155
Leu Leu Leu Cys Pro Cys Ala Pro Glu	Asp Ala Gly Cys Gly Glu Arg		
165	170		175
Arg Arg Asn Thr Ile Ala Pro Ser Cys	Ala Leu Pro Ser Val Thr Pro		
180	185		190
Asn Cys Leu Asp Leu Arg Ser Phe Cys	Arg Ala Asp Pro Leu Cys Arg		
195	200		205
Ser Arg Leu Met Asp Phe Gln Thr His	Cys His Pro Met Asp Ile Leu		
210	215		220
Gly Thr Cys Ala Thr Glu Gln Ser Arg	Cys Leu Arg Ala Tyr Leu Gly		
225	230		235
Leu Ile Gly Thr Ala Met Thr Pro Asn	Phe Ile Ser Lys Val Asn Thr		
245	250		255
Thr Val Ala Leu Ser Cys Thr Cys Arg	Gly Ser Gly Asn Leu Gln Asp		
260	265		270
Glu Cys Glu Gln Leu Glu Arg Ser Phe	Ser Gln Asn Pro Cys Leu Val		
275	280		285
Glu Ala Ile Ala Ala Lys Met Arg Phe	His Arg Gln Leu Phe Ser Gln		
290	295		300
Asp Trp Ala Asp Ser Thr Phe Ser Val	Val Gln Gln Gln Asn Ser Asn		
305	310		315
Pro Ala Leu Arg Leu Gln Pro Arg Leu	Pro Ile Leu Ser Phe Ser Ile		
325	330		335
Leu Pro Leu Ile Leu Leu Gln Thr Leu	Trp		
340	345		

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1889 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS
(B) LOCATION: 41..1231

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

```
55 CGCAGGCAGA GCGCTGTCGC ATCCCGGGCG TCCACCCGCC ATG GGG CTC TCC TGG
Met Gly Leu Ser Trp
350

103 AGC CCG CGA CCT CCA CTG CTG ATG ATC CTG CTA CTG GTG CTG TCG TTG
Ser Pro Arg Pro Pro Leu Leu Met Ile Leu Leu Leu Val Leu Ser Leu
355 360 365

151 TGG CTG CCA CTT GGA GCA GGA AAC TCC CTT GCC ACA GAG AAC AGG TTT
Trp Leu Pro Leu Gly Ala Gly Asn Ser Leu Ala Thr Glu Asn Arg Phe
370 375 380

199 GTG AAC AGC TGT ACC CAG GCC AGA AAG AAA TGC GAG GCT AAT CCC GCT
Val Asn Ser Cys Thr Gln Ala Arg Lys Lys Cys Glu Ala Asn Pro Ala
385 390 395

247 TGC AAG GCT GCC TAC CAG CAC CTG GGC TCC TGC ACC TCC AGT TTA AGC
Cys Lys Ala Ala Tyr Gln His Leu Gly Ser Cys Thr Ser Ser Leu Ser
400 405 410 415

295 AGG CCG CTG CCC TTA GAG GAG TCT GCC ATG TCT GCA GAC TGC CTA GAG
Arg Pro Leu Pro Leu Glu Glu Ser Ala Met Ser Ala Asp Cys Leu Glu
420 425 430

343 GCA GCA GAA CAA CTC AGG AAC AGC TCT CTG ATA GAC TGC AGG TGC CAT
Ala Ala Glu Gln Leu Arg Asn Ser Ser Leu Ile Asp Cys Arg Cys His
435 440 445

391 CGG CGC ATG AAG CAC CAA GCT ACC TGT CTG GAC ATT TAT TGG ACC GTT
Arg Arg Met Lys His Gln Ala Thr Cys Leu Asp Ile Tyr Trp Thr Val
450 455 460

439 CAC CCT GCC CGA AGC CTT GGT GAC TAC GAG TTG GAT GTC TCA CCC TAT
His Pro Ala Arg Ser Leu Gly Asp Tyr Glu Leu Asp Val Ser Pro Tyr
465 470 475

487 GAA GAC ACA GTG ACC AGC AAA CCC TGG AAA ATG AAT CTT AGC AAG TTG
Glu Asp Thr Val Thr Ser Lys Pro Trp Lys Met Asn Leu Ser Lys Leu
480 485 490 495

535 AAC ATG CTC AAA CCA GAC TCG GAC CTC TGC CTC AAA TTT GCT ATG CTG
Asn Met Leu Lys Pro Asp Ser Asp Leu Cys Leu Lys Phe Ala Met Leu
500 505 510 515

583 TGT ACT CTT CAC GAC AAG TGT GAC CGC CTG CGC AAG GCC TAC GGG GAG
Cys Thr Leu His Asp Lys Cys Asp Arg Leu Arg Lys Ala Tyr Gly Glu
515 520 525
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631 GCA TGC TCA GGG ATC CGC TGC CAG CGC CAC CTC TGC CTA GCC CAG CTG
 Ala Cys Ser Gly Ile Arg Cys Gln Arg His Leu Cys Leu Ala Gln Leu
 530 535 540

679 CGC TCC TTC TTT GAG AAG GCA GCA GAG TCC CAC GCT CAG GGT CTG CTG
 Arg Ser Phe Phe Glu Lys Ala Ala Glu Ser His Ala Gln Gly Leu Leu
 545 550 555

727 CTG TGT CCC TGT GCA CCA GAA GAT GCG GGC TGT GGG GAG CGG CGG CGT
 Leu Cys Pro Cys Ala Pro Glu Asp Ala Gly Cys Gly Glu Arg Arg Arg
 560 565 570 575

775 AAC ACC ATC GCC CCC AGT TGC GCC CTG CCT TCT GTA ACC CCC AAT TGC
 Asn Thr Ile Ala Pro Ser Cys Ala Leu Pro Ser Val Thr Pro Asn Cys
 580 585 590

823 CTG GAT CTG CGG AGC TTC TGC CGT GCG GAC CCT TTG TGC AGA TCA CGC
 Leu Asp Leu Arg Ser Phe Cys Arg Ala Asp Pro Leu Cys Arg Ser Arg
 595 600 605

871 CTG ATG GAC TTC CAG ACC CAC TGT CAT CCT ATG GAC ATC CTT GGG ACT
 Leu Met Asp Phe Gln Thr His Cys His Pro Met Asp Ile Leu Gly Thr
 610 615 620

919 TGT GCA ACT GAG CAG TCC AGA TGT CTG CGG GCA TAC CTG GGG CTG ATT
 Cys Ala Thr Glu Gln Ser Arg Cys Leu Arg Ala Tyr Leu Gly Leu Ile
 625 630 635

967 GGG ACT GCC ATG ACC CCA AAC TTC ATC AGC AAG GTC AAC ACT ACT GTT
 Gly Thr Ala Met Thr Pro Asn Phe Ile Ser Lys Val Asn Thr Thr Val
 640 645 650 655

1015 GCC TTA AGC TGC ACC TGC CGA GGC AGC GGC AAC CTA CAG GAC GAG TGT
 Ala Leu Ser Cys Thr Cys Arg Gly Ser Gly Asn Leu Gln Asp Glu Cys
 660 665 670

1063 GAA CAG CTG GAA AGG TCC TTC TCC CAG AAC CCC TGC CTC GTG GAG GCC
 Glu Gln Leu Glu Arg Ser Phe Ser Gln Asn Pro Cys Leu Val Glu Ala
 675 680 685

1111 ATT GCA GCT AAG ATG CGT TTC CAC AGA CAG CTC TTC TCC CAG GAC TGG
 Ile Ala Ala Lys Met Arg Phe His Arg Gln Leu Phe Ser Gln Asp Trp
 690 695 700

1159 GCA GAC TCT ACT TTT TCA GTG GTG CAG CAG CAG AAC AGC AAC CCT GCT
 Ala Asp Ser Thr Phe Ser Val Val Gln Gln Gln Asn Ser Asn Pro Ala
 705 710 715

1207 CTG AGA CTG CAG CCC AGG CTA CCC ATT CTT TCT TTC TCC ATC CTT CCC
 Leu Arg Leu Gln Pro Arg Leu Pro Ile Leu Ser Phe Ser Ile Leu Pro
 720 725 730 735

1261 TTG ATT CTG CTG CAG ACC CTC TGG TAGCTGGGCT TCCTCAGGGT CCTTTGTCCT
 Leu Ile Leu Leu Gln Thr Leu Trp
 740
 1321 CTCACACCACA CCCAGACTGA TTTGCAGCCT GTGGTGGGAG AGAACTCGCC AGCCTGTGGA
 1381 AGAAGACGCA GCGTGCTACA CAGCAACCCG GAACCAACCA GGCATTCCGC AGCACATCCC
 1441 GTCTGCTCCA GAAGAGGTCT TAGAAGTGAG GGCTGTGACC CTTCCGATCC TGAGCGGCTA
 1501 GTTTTCAAAC CTCCCTTGCC CCTGCTTCCT TCTGGCTCAG GCTGCTCCTC CTTAGGACTT
 1561 TGTGGGTCCA GTTTTCCTT CTGTTCTGAT GGTGATTAGC GGCTCACCTC CAGCGCTTCT
 1621 TCCTGTTTCC CAGGACCACC CAGAGGCTAA GGAATCAGTC ATTCCCTGTT GCCTTCTCCA
 1681 GGAAGGCAGG CTAAGGGTTC TGAGGTGACT GAGAAAAATG TTTCCTTTGT GTGGAAGGCT
 1741 GGTGCTCCAG CCTCCACGTC CCTCTGAATG GAAGATAAAA ACCTGCTGGT GTCTTGACTG
 1801 CTCTGCCAGG CAATCCTGAA CATTTGGGCA TGAAGAGCTA AAGTCTTTGG GTCTTGTTTA
 1861 ACTCTATTA CTGTCCCCAA ATTCCCCTAG TCCCTGGGT CATGATTAAA CATTTTGACT
 1889 TAAAAAAAAA AAAAAAAAAA AAAAAAAA

(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 397 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Met	Gly	Leu	Ser	Trp	Ser	Pro	Arg	Pro	Pro	Leu	Leu	Met	Ile	Leu	Leu
1				5					10					15	
Leu	Val	Leu	Ser	Leu	Trp	Leu	Pro	Leu	Gly	Ala	Gly	Asn	Ser	Leu	Ala
			20					25					30		
Thr	Glu	Asn	Arg	Phe	Val	Asn	Ser	Cys	Thr	Gln	Ala	Arg	Lys	Lys	Cys
		35					40					45			
Glu	Ala	Asn	Pro	Ala	Cys	Lys	Ala	Ala	Tyr	Gln	His	Leu	Gly	Ser	Cys
	50					55				60					
Thr	Ser	Ser	Leu	Ser	Arg	Pro	Leu	Pro	Leu	Glu	Glu	Ser	Ala	Met	Ser
65					70					75				80	

Ala Asp Cys Leu Glu Ala Ala Glu Gln Leu Arg Asn Ser Ser Leu Ile
 85 90 95
 Asp Cys Arg Cys His Arg Arg Met Lys His Gln Ala Thr Cys Leu Asp
 100 105 110
 Ile Tyr Trp Thr Val His Pro Ala Arg Ser Leu Gly Asp Tyr Glu Leu
 115 120 125
 Asp Val Ser Pro Tyr Glu Asp Thr Val Thr Ser Lys Pro Trp Lys Met
 130 135 140
 Asn Leu Ser Lys Leu Asn Met Leu Lys Pro Asp Ser Asp Leu Cys Leu
 145 150 155 160
 Lys Phe Ala Met Leu Cys Thr Leu His Asp Lys Cys Asp Arg Leu Arg
 165 170 175
 Lys Ala Tyr Gly Glu Ala Cys Ser Gly Ile Arg Cys Gln Arg His Leu
 180 185 190
 Cys Leu Ala Gln Leu Arg Ser Phe Phe Glu Lys Ala Ala Glu Ser His
 195 200 205
 Ala Gln Gly Leu Leu Leu Cys Pro Cys Ala Pro Glu Asp Ala Gly Cys
 210 215 220
 Gly Glu Arg Arg Arg Asn Thr Ile Ala Pro Ser Cys Ala Leu Pro Ser
 225 230 235 240
 Val Thr Pro Asn Cys Leu Asp Leu Arg Ser Phe Cys Arg Ala Asp Pro
 245 250 255
 Leu Cys Arg Ser Arg Leu Met Asp Phe Gln Thr His Cys His Pro Met
 260 265 270
 Asp Ile Leu Gly Thr Cys Ala Thr Glu Gln Ser Arg Cys Leu Arg Ala
 275 280 285
 Tyr Leu Gly Leu Ile Gly Thr Ala Met Thr Pro Asn Phe Ile Ser Lys
 290 295 300
 Val Asn Thr Thr Val Ala Leu Ser Cys Thr Cys Arg Gly Ser Gly Asn
 305 310 315 320
 Leu Gln Asp Glu Cys Glu Gln Leu Glu Arg Ser Phe Ser Gln Asn Pro
 325 330 335
 Cys Leu Val Glu Ala Ile Ala Ala Lys Met Arg Phe His Arg Gln Leu
 340 345 350
 Phe Ser Gln Asp Trp Ala Asp Ser Thr Phe Ser Val Val Gln Gln Gln
 355 360 365
 Asn Ser Asn Pro Ala Leu Arg Leu Gln Pro Arg Leu Pro Ile Leu Ser
 370 375 380
 Phe Ser Ile Leu Pro Leu Ile Leu Leu Gln Thr Leu Trp
 385 390 395

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1271 base pairs

46	C	GGC	TAC	TGT	GAA	ACA	CCT	CAA	CTC	AGG	AAC	AGC	TCT	CTG	ATA	GGC	
	Gly	Tyr	Cys	Glu	Thr	Pro	Gln	Leu	Arg	Asn	Ser	Ser	Leu	Ile	Gly		
			400					405						410			
94	TGC	ATG	TGC	CAC	CGG	CGC	ATG	AAG	AAC	CAG	GTT	GCC	TGC	TTG	GAC	ATC	
	Cys	Met	Cys	His	Arg	Arg	Met	Lys	Asn	Gln	Val	Ala	Cys	Leu	Asp	Ile	
			415					420					425				
142	TAT	TGG	ACC	GTT	CAC	CGT	GCC	CGC	AGC	CTT	GGT	AAC	TAT	GAG	CTG	GAT	
	Tyr	Trp	Thr	Val	His	Arg	Ala	Arg	Ser	Leu	Gly	Asn	Tyr	Glu	Leu	Asp	
		430					435					440					
190	GTC	TCC	CCC	TAT	GAA	GAC	ACA	GTG	ACC	AGC	AAA	CCC	TGG	AAA	ATG	AAT	
	Val	Ser	Pro	Tyr	Glu	Asp	Thr	Val	Thr	Ser	Lys	Pro	Trp	Lys	Met	Asn	
		445				450					455					460	
238	CTC	AGC	AAA	CTG	AAC	ATG	CTC	AAA	CCA	GAC	TCA	GAC	CTC	TGC	CTC	AAG	
	Leu	Ser	Lys	Leu	Asn	Met	Leu	Lys	Pro	Asp	Ser	Asp	Leu	Cys	Leu	Lys	
					465					470					475		
286	TTT	GCC	ATG	CTG	TGT	ACT	CTC	AAT	GAC	AAG	TGT	GAC	CGG	CTG	CGC	AAG	
	Phe	Ala	Met	Leu	Cys	Thr	Leu	Asn	Asp	Lys	Cys	Asp	Arg	Leu	Arg	Lys	
				480					485					490			
334	GCC	TAC	GGG	GAG	GCG	TGC	TCC	GGG	CCC	CAC	TGC	CAG	CGC	CAC	GTC	TGC	
	Ala	Tyr	Gly	Glu	Ala	Cys	Ser	Gly	Pro	His	Cys	Gln	Arg	His	Val	Cys	
			495					500					505				
382	CTC	AGG	CAG	CTG	CTC	ACT	TTC	TTC	GAG	AAG	GCC	GCC	GAG	CCC	CAC	GCG	
	Leu	Arg	Gln	Leu	Leu	Thr	Phe	Phe	Glu	Lys	Ala	Ala	Glu	Pro	His	Ala	
		510					515					520					
430	CAG	GGC	CTG	CTA	CTG	TGC	CCA	TGT	GCC	CCC	AAC	GAC	CGG	GGC	TGC	GGG	
	Gln	Gly	Leu	Leu	Leu	Cys	Pro	Cys	Ala	Pro	Asn	Asp	Arg	Gly	Cys	Gly	
		525				530					535					540	
478	GAG	CGC	CGG	CGC	AAC	ACC	ATC	GCC	CCC	AAC	TGC	GCG	CTG	CCG	CCT	GTG	
	Glu	Arg	Arg	Arg	Asn	Thr	Ile	Ala	Pro	Asn	Cys	Ala	Leu	Pro	Pro	Val	
					545					550					555		

526 GCC CCC AAC TGC CTG GAG CTG CGG CGC CTC TGC TTC TCC GAC CCG CTT
 Ala Pro Asn Cys Leu Glu Leu Arg Arg Leu Cys Phe Ser Asp Pro Leu
 560 565 570

574 TGC AGA TCA CGC CTG GTG GAT TTC CAG ACC CAC TGC CAT CCC ATG GAC
 Cys Arg Ser Arg Leu Val Asp Phe Gln Thr His Cys His Pro Met Asp
 575 580 585

622 ATC CTA GGA ACT TGT GCA ACA GAG CAG TCC AGA TGT CTA CGA GCA TAC
 Ile Leu Gly Thr Cys Ala Thr Glu Gln Ser Arg Cys Leu Arg Ala Tyr
 590 595 600

670 CTG GGG CTG ATT GGG ACT GCC ATG ACC CCC AAC TTT GTC AGC AAT GTC
 Leu Gly Leu Ile Gly Thr Ala Met Thr Pro Asn Phe Val Ser Asn Val
 605 610 615 620

718 AAC ACC AGT GTT GCC TTA AGC TGC ACC TGC CGA GGC AGT GGC AAC CTG
 Asn Thr Ser Val Ala Leu Ser Cys Thr Cys Arg Gly Ser Gly Asn Leu
 625 630 635

766 CAG GAG GAG TGT GAA ATG CTG GAA GGG TTC TTC TCC CAC AAC CCC TGC
 Gln Glu Glu Cys Glu Met Leu Glu Gly Phe Phe Ser His Asn Pro Cys
 640 645 650

814 CTC ACG GAG GCC ATT GCA GCT AAG ATG CGT TTT CAC AGC CAA CTC TTC
 Leu Thr Glu Ala Ile Ala Ala Lys Met Arg Phe His Ser Gln Leu Phe
 655 660 665

862 TCC CAG GAC TGG CCA CAC CCT ACC TTT GCT GTG ATG GCA CAC CAG AAT
 Ser Gln Asp Trp Pro His Pro Thr Phe Ala Val Met Ala His Gln Asn
 670 675 680

910 GAA AAC CCT GCT GTG AGG CCA CAG CCC TGG GTG CCC TCT CTT TTC TCC
 Glu Asn Pro Ala Val Arg Pro Gln Pro Trp Val Pro Ser Leu Phe Ser
 685 690 695 700

956 TGC ACG CTT CCC TTG ATT CTG CTC CTG AGC CTA TGG TAGCTGGACT
 Cys Thr Leu Pro Leu Ile Leu Leu Leu Ser Leu Trp
 705 710

1016 TCCCCAGGGC CCTCTTCCCC TCCACCACAC CCAGGTGGAC TTGCAGCCCA CAAGGGGTGA

1076 GGAAAGGACA GCAGCAGGAA GGAGGTGCAG TGCGCAGATG AGGGCACAGG AGAAGCTAAG

1136 GGTTATGACC TCCAGATCCT TACTGGTCCA GTCCTCATTC CCTCCACCCC ATCTCCACTT

1196 CTGATTCATG CTGCCCCCTC TTGGTGGCCA CAATTTAGCC ATGTCATCTG GTGCCTGTGG

1256 GCCTTGCTTT ATTCCTATTA TTGTCCTAAA GTCTCTCTGG GCTCTTGGAT CATGATTAAA

(2) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 315 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

Gly	Tyr	Cys	Glu	Thr	Pro	Gln	Leu	Arg	Asn	Ser	Ser	Leu	Ile	Gly	Cys	1	5	10	15
Met	Cys	His	Arg	Arg	Met	Lys	Asn	Gln	Val	Ala	Cys	Leu	Asp	Ile	Tyr	20	25	30	
Trp	Thr	Val	His	Arg	Ala	Arg	Ser	Leu	Gly	Asn	Tyr	Glu	Leu	Asp	Val	35	40	45	
Ser	Pro	Tyr	Glu	Asp	Thr	Val	Thr	Ser	Lys	Pro	Trp	Lys	Met	Asn	Leu	50	55	60	
Ser	Lys	Leu	Asn	Met	Leu	Lys	Pro	Asp	Ser	Asp	Leu	Cys	Leu	Lys	Phe	65	70	75	80
Ala	Met	Leu	Cys	Thr	Leu	Asn	Asp	Lys	Cys	Asp	Arg	Leu	Arg	Lys	Ala	85	90	95	
Tyr	Gly	Glu	Ala	Cys	Ser	Gly	Pro	His	Cys	Gln	Arg	His	Val	Cys	Leu	100	105	110	
Arg	Gln	Leu	Leu	Thr	Phe	Phe	Glu	Lys	Ala	Ala	Glu	Pro	His	Ala	Gln	115	120	125	
Gly	Leu	Leu	Cys	Pro	Cys	Ala	Pro	Asn	Asp	Arg	Gly	Cys	Gly	Glu	130	135	140		
Arg	Arg	Arg	Asn	Thr	Ile	Ala	Pro	Asn	Cys	Ala	Leu	Pro	Pro	Val	Ala	145	150	155	160
Pro	Asn	Cys	Leu	Glu	Leu	Arg	Arg	Leu	Cys	Phe	Ser	Asp	Pro	Leu	Cys	165	170	175	
Arg	Ser	Arg	Leu	Val	Asp	Phe	Gln	Thr	His	Cys	His	Pro	Met	Asp	Ile	180	185	190	
Leu	Gly	Thr	Cys	Ala	Thr	Glu	Gln	Ser	Arg	Cys	Leu	Arg	Ala	Tyr	Leu	195	200	205	
Gly	Leu	Ile	Gly	Thr	Ala	Met	Thr	Pro	Asn	Phe	Val	Ser	Asn	Val	Asn	210	215	220	
Thr	Ser	Val	Ala	Leu	Ser	Cys	Thr	Cys	Arg	Gly	Ser	Gly	Asn	Leu	Gln	225	230	235	240
Glu	Glu	Cys	Glu	Met	Leu	Glu	Gly	Phe	Phe	Ser	His	Asn	Pro	Cys	Leu	245	250	255	
Thr	Glu	Ala	Ile	Ala	Ala	Lys	Met	Arg	Phe	His	Ser	Gln	Leu	Phe	Ser	260	265	270	

Gln Asp Trp Pro His Pro Thr Phe Ala Val Met Ala His Gln Asn Glu
 275 280 285

Asn Pro Ala Val Arg Pro Gln Pro Trp Val Pro Ser Leu Phe Ser Cys
 290 295 300

Thr Leu Pro Leu Ile Leu Leu Ser Leu Trp
 305 310 315

(2) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1699 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 175..1374

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

60 TGTGGACGCG CGCTTCGGAG TTGGAGGGCG GCGCCAGGA CCCTGGTGGG AGAGTGTGTG

120 CGTCGCGCTG GAGGGCGGGA GGCGGGGGCG GGAGGTGCCG GTCGAGGGAG CCCCCTCTC

177 AGAGCTCCAG GGGAGGAGCG AGGGGAGCGC GGAGCCCGGC GCCTACAGCT CGCC ATG
 Met

225 GTG CGC CCC CTG AAC CCG CGA CCG CTG CCG CCC GTA GTC CTG ATG TTG

Val Arg Pro Leu Asn Pro Arg Pro Leu Pro Pro Val Val Leu Met Leu
 320 325 330

273 CTG CTG CTG CTG CCG CCG TCG CCG CTG CCT CTC GCA GCC GGA GAC CCC

Leu Leu Leu Leu Pro Pro Ser Pro Leu Pro Leu Ala Ala Gly Asp Pro
 335 340 345

321 CTT CCC ACA GAA AGC CGA CTC ATG AAC AGC TGT CTC CAG GCC AGG AGG

Leu Pro Thr Glu Ser Arg Leu Met Asn Ser Cys Leu Gln Ala Arg Arg
 350 355 360

369 AAG TGC CAG GCT GAT CCC ACC TGC AGT GCT GCC TAC CAC CAC CTG GAT

Lys Cys Gln Ala Asp Pro Thr Cys Ser Ala Ala Tyr His His Leu Asp
 365 370 375 380

417 TCC TGC ACC TCT AGC ATA AGC ACC CCA CTG CCC TCA GAG GAG CCT TCG

Ser Cys Thr Ser Ser Ile Ser Thr Pro Leu Pro Ser Glu Glu Pro Ser
 385 390 395

465 GTC CCT GCT GAC TGC CTG GAG GCA GCA CAG CAA CTC AGG AAC AGC TCT
 Val Pro Ala Asp Cys Leu Glu Ala Ala Gln Gln Leu Arg Asn Ser Ser
 400 405 410

513 CTG ATA GGC TGC ATG TGC CAC CGG CGC ATG AAG AAC CAG GTT GCC TGC
 Leu Ile Gly Cys Met Cys His Arg Arg Met Lys Asn Gln Val Ala Cys
 415 420 425

561 TTG GAC ATC TAT TGG ACC GTT CAC CGT GCC CGC AGC CTT GGT AAC TAT
 Leu Asp Ile Tyr Trp Thr Val His Arg Ala Arg Ser Leu Gly Asn Tyr
 430 435 440

609 GAG CTG GAT GTC TCC CCC TAT GAA GAC ACA GTG ACC AGC AAA CCC TGG
 Glu Leu Asp Val Ser Pro Tyr Glu Asp Thr Val Thr Ser Lys Pro Trp
 445 450 455 460

657 AAA ATG AAT CTC AGC AAA CTG AAC ATG CTC AAA CCA GAC TCA GAC CTC
 Lys Met Asn Leu Ser Lys Leu Asn Met Leu Lys Pro Asp Ser Asp Leu
 465 470 475

705 TGC CTC AAG TTT GCC ATG CTG TGT ACT CTC AAT GAC AAG TGT GAC CGG
 Cys Leu Lys Phe Ala Met Leu Cys Thr Leu Asn Asp Lys Cys Asp Arg
 480 485 490

753 CTG CGC AAG GCC TAC GGG GAG GCG TGC TCC GGG CCC CAC TGC CAG CGC
 Leu Arg Lys Ala Tyr Gly Glu Ala Cys Ser Gly Pro His Cys Gln Arg
 495 500 505

801 CAC GTC TGC CTC AGG CAG CTG CTC ACT TTC TTC GAG AAG GCC GCC GAG
 His Val Cys Leu Arg Gln Leu Leu Thr Phe Phe Glu Lys Ala Ala Glu
 510 515 520

849 CCC CAC GCG CAG GGC CTG CTA CTG TGC CCA TGT GCC CCC AAC GAC CGG
 Pro His Ala Gln Gly Leu Leu Leu Cys Pro Cys Ala Pro Asn Asp Arg
 525 530 535 540

897 GGC TGC GGG GAG CGC CGG CGC AAC ACC ATC GCC CCC AAC TGC GCG CTG
 Gly Cys Gly Glu Arg Arg Arg Asn Thr Ile Ala Pro Asn Cys Ala Leu
 545 550 555

945 CCG CCT GTG GCC CCC AAC TGC CTG GAG CTG CGG CGC CTC TGC TTC TCC
 Pro Pro Val Ala Pro Asn Cys Leu Glu Leu Arg Arg Leu Cys Phe Ser
 560 565 570

993 GAC CCG CTT TGC AGA TCA CGC CTG GTG GAT TTC CAG ACC CAC TGC CAT
 Asp Pro Leu Cys Arg Ser Arg Leu Val Asp Phe Gln Thr His Cys His
 575 580 585

1041 CCC ATG GAC ATC CTA GGA ACT TGT GCA ACA GAG CAG TCC AGA TGT CTA
 Pro Met Asp Ile Leu Gly Thr Cys Ala Thr Glu Gln Ser Arg Cys Leu
 590 595 600

1089 CGA GCA TAC CTG GGG CTG ATT GGG ACT GCC ATG ACC CCC AAC TTT GTC
 Arg Ala Tyr Leu Gly Leu Ile Gly Thr Ala Met Thr Pro Asn Phe Val
 605 610 615 620
 1137 AGC AAT GTC AAC ACC AGT GTT GCC TTA AGC TGC ACC TGC CGA GGC AGT
 Ser Asn Val Asn Thr Ser Val Ala Leu Ser Cys Thr Cys Arg Gly Ser
 625 630 635
 1185 GGC AAC CTG CAG GAG GAG TGT GAA ATG CTG GAA GGG TTC TTC TCC CAC
 Gly Asn Leu Gln Glu Glu Cys Glu Met Leu Glu Gly Phe Phe Ser His
 640 645 650
 1233 AAC CCC TGC CTC ACG GAG GCC ATT GCA GCT AAG ATG CGT TTT CAC AGC
 Asn Pro Cys Leu Thr Glu Ala Ile Ala Ala Lys Met Arg Phe His Ser
 655 660 665
 1281 CAA CTC TTC TCC CAG GAC TGG CCA CAC CCT ACC TTT GCT GTG ATG GCA
 Gln Leu Phe Ser Gln Asp Trp Pro His Pro Thr Phe Ala Val Met Ala
 670 675 680
 1329 CAC CAG AAT GAA AAC CCT GCT GTG AGG CCA CAG CCC TGG GTG CCC TCT
 His Gln Asn Glu Asn Pro Ala Val Arg Pro Gln Pro Trp Val Pro Ser
 685 690 695 700
 1374 CTT TTC TCC TGC ACG CTT CCC TTG ATT CTG CTC CTG AGC CTA TGG
 Leu Phe Ser Cys Thr Leu Pro Leu Ile Leu Leu Leu Ser Leu Trp
 705 710 715
 1434 TAGCTGGACT TCCCCAGGGC CCTCTTCCCC TCCACCACAC CCAGGTGGAC TTGCAGCCCA
 1494 CAAGGGGTGA GGAAAGGACA GCAGCAGGAA GGAGGTGCAG TGCGCAGATG AGGGCACAGG
 1554 AGAAGCTAAG GGTATGACC TCCAGATCCT TACTGGTCCA GTCCTCATTC CCTCCACCCC
 1614 ATCTCCACTT CTGATTCATG CTGCCCCTCC TTGGTGGCCA CAATTTAGCC ATGTCATCTG
 1674 GTGCCTGTGG GCCTTGCTTT ATTCCTATTA TTGTCCTAAA GTCTCTCTGG GCTCTTGGAT
 1699 CATGATTAAA CCTTTGACTT AAAAA

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

Met Val Arg Pro Leu Asn Pro Arg Pro Leu Pro Pro Val Val Leu Met
 1 5 10 15
 Leu Leu Leu Leu Leu Pro Pro Ser Pro Leu Pro Leu Ala Ala Gly Asp
 20 25 30
 Pro Leu Pro Thr Glu Ser Arg Leu Met Asn Ser Cys Leu Gln Ala Arg
 35 40 45
 Arg Lys Cys Gln Ala Asp Pro Thr Cys Ser Ala Ala Tyr His His Leu
 50 55 60
 Asp Ser Cys Thr Ser Ser Ile Ser Thr Pro Leu Pro Ser Glu Glu Pro
 65 70 75 80
 Ser Val Pro Ala Asp Cys Leu Glu Ala Ala Gln Gln Leu Arg Asn Ser
 85 90 95
 Ser Leu Ile Gly Cys Met Cys His Arg Arg Met Lys Asn Gln Val Ala
 100 105 110
 Cys Leu Asp Ile Tyr Trp Thr Val His Arg Ala Arg Ser Leu Gly Asn
 115 120 125
 Tyr Glu Leu Asp Val Ser Pro Tyr Glu Asp Thr Val Thr Ser Lys Pro
 130 135 140
 Trp Lys Met Asn Leu Ser Lys Leu Asn Met Leu Lys Pro Asp Ser Asp
 145 150 155 160
 Leu Cys Leu Lys Phe Ala Met Leu Cys Thr Leu Asn Asp Lys Cys Asp
 165 170 175
 Arg Leu Arg Lys Ala Tyr Gly Glu Ala Cys Ser Gly Pro His Cys Gln
 180 185 190
 Arg His Val Cys Leu Arg Gln Leu Leu Thr Phe Phe Glu Lys Ala Ala
 195 200 205
 Glu Pro His Ala Gln Gly Leu Leu Leu Cys Pro Cys Ala Pro Asn Asp
 210 215 220
 Arg Gly Cys Gly Glu Arg Arg Arg Asn Thr Ile Ala Pro Asn Cys Ala
 225 230 235 240
 Leu Pro Pro Val Ala Pro Asn Cys Leu Glu Leu Arg Arg Leu Cys Phe
 245 250 255
 Ser Asp Pro Leu Cys Arg Ser Arg Leu Val Asp Phe Gln Thr His Cys
 260 265 270
 His Pro Met Asp Ile Leu Gly Thr Cys Ala Thr Glu Gln Ser Arg Cys
 275 280 285
 Leu Arg Ala Tyr Leu Gly Leu Ile Gly Thr Ala Met Thr Pro Asn Phe
 290 295 300
 Val Ser Asn Val Asn Thr Ser Val Ala Leu Ser Cys Thr Cys Arg Gly
 305 310 315 320
 Ser Gly Asn Leu Gln Glu Glu Cys Glu Met Leu Glu Gly Phe Phe Ser
 325 330 335
 His Asn Pro Cys Leu Thr Glu Ala Ile Ala Ala Lys Met Arg Phe His
 340 345 350

Ser	Gln	Leu	Phe	Ser	Gln	Asp	Trp	Pro	His	Pro	Thr	Phe	Ala	Val	Met
		355					360					365			
Ala	His	Gln	Asn	Glu	Asn	Pro	Ala	Val	Arg	Pro	Gln	Pro	Trp	Val	Pro
	370					375					380				
Ser	Leu	Phe	Ser	Cys	Thr	Leu	Pro	Leu	Ile	Leu	Leu	Leu	Ser	Leu	Trp
385					390					395					400